

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 06:48:07 : Search time 3020 Seconds

(without alignments)  
10417.263 Million cell updates/sec

Title: US-10-010-568-1

Perfect score: 1081

Sequence: 1 catattgccaaactgaactc.....ccttgaataatcttacc 1081

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

GenBank:\*

1: gb\_ba:\*

2: gb\_hlg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_by:\*

13: gb\_un:\*

14: gb\_vl:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_vl:\*

30: em\_hlg\_hum:\*

31: em\_hlg\_inv:\*

32: em\_hlg\_other:\*

33: em\_hlg\_mus:\*

34: em\_hlg\_pln:\*

35: em\_hlg\_rod:\*

36: em\_hlg\_mam:\*

37: em\_hlg\_vrt:\*

38: em\_ay:\*

39: em\_hlgo\_hum:\*

40: em\_hlgo\_mus:\*

41: em\_hlgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1081	100.0	1081	6	AX458238
2	1081	100.0	1414	6	AB065877
3	1081	100.0	9905	6	AX379470
4	1081	100.0	67645	9	AL356486
5	1081	100.0	156555	9	AC026756
6	1079.4	99.9	1729	6	AX191332
7	1046	96.8	1092	6	AF370886
8	1014	93.8	1014	6	AX148186
9	1014	93.8	1014	6	AX379468
10	1014	93.8	1014	6	AX384211
11	1014	93.8	1014	9	AB083598
12	1014	93.8	1014	9	AF411109
13	1012.4	93.7	1014	6	AX305130
14	1012.4	93.7	1014	6	AX464561
15	980.8	90.7	1020	6	AX147840
16	769	71.1	202938	2	AC108794
17	538.8	49.8	578	6	AX147814
18	385	35.6	2245	6	AX384210
19	242	22.4	657	6	AX244775
20	161.2	14.9	1977	5	AF031897
21	158.6	14.7	1293	10	MMW22829
22	158.6	14.7	3204	10	RN022830
23	153.8	14.2	12630	2	MMW24536
24	153.8	14.2	288763	2	AC124692
25	150.2	13.9	1312	9	S81950
26	150.2	13.9	1426	9	HSU42029
27	150.2	13.9	2424	9	HSU42030
28	150.2	13.9	16178	9	HSU4569
29	150.2	13.9	176170	2	AC021662
30	150.2	13.9	176251	9	AC013251
31	147.6	13.7	73949	2	AC105795
32	147	13.6	1308	4	BTU34041
33	147	13.6	1666	4	BTU34041
34	145.8	13.5	2231	5	AF242850
35	144.6	13.4	2951	5	AF432354
36	134.8	12.5	1163	5	GDP2Y3
37	134.2	12.4	3055	11	HSATPRMR
38	134.2	12.4	3055	11	G28604
39	134.2	12.4	136930	5	AL590151
40	133.2	12.3	1074	5	AF069555
41	131.4	12.2	91107	2	AC116265
42	131.4	12.2	192524	2	AC120742
43	131.2	12.1	1325	9	AF247785
44	131.2	12.1	1380	9	AF348078
45	131.2	12.1	1449	9	BC030948

## ALIGNMENTS

RESULT 1

AX458238

LOCUS AX458238 1081 bp DNA linear PAT 08-JUL-2002

DEFINITION Sequence 1 from Patent WO0246414.

ACCESSION AX458238

VERSION AX458238.1 GI:21724972

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Ramanathan, C., Feder, J., Nelson, T., Cacace, A., Barber, L. and Rysek, R.P.

TITLE A novel human g-protein coupled receptor, hgrbm22, expressed

```

/codon_start=-1
/evidence=not experimental
/product="seven transmembrane helix receptor"
/protein_id="BAC06095.1"
/db_xref="GI:21929019"
/translation="MNEPDLVLANSDPFDYAAFGNCTDENIPLKHYLPVYGIIF
LVGPENAVVISTYIFRMKPKSSTIMMIACTDLYLPLHYVSGEMWIFG
DMWCKIRSFENLYSILFLPCPSIFRVLHPSGSIHTRCAVAVAVWII
SLVAVIPMFELTSTNRNNSACLDLSDSELMITKYNILIRATPECLPIVITLCY
TTIHTLHGLDIOISCKOKARBLTILLALFVCPPLPHILVIRIRESLTLISCSI
ENQIHAYIVSRPLALNLTGNLILYVSDNFQAVGSTRCKVSNLEQAKKISTIS
NNP"
BASE COUNT      376 a      337 c      260 g      441 t
ORIGIN
Query Match      100.0%; Score 1081; DB 9; Length 1414;
Best Local Similarity 100.0%; Pred. No. 9,3e-271;
Matches 1081; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATATTGCCAACTGAAGTCTCTGTTTCTTGCAAGATGAAGAGCAACATGAATG 60
Db 148 CATATTGCCAACTGAAGTCTCTGTTTCTTGCAAGATGAAGAGCAACATGAATG 207

QY 61 AGCCACTAGACTATTAGCAATGCTTCTGATTTCCCGATTATGACGCTCTTTGGAA 120
Db 208 AGCCACTAGACTATTAGCAATGCTTCTGATTTCCCGATTATGACGCTCTTTGGAA 267

QY 121 ATTGCACTGATGAAACATGCCACTCAAGATGCACTACCTCCCTGTTATTTATGGCATTA 180
Db 268 ATTGCACTGATGAAACATGCCACTCAAGATGCACTACCTCCCTGTTATTTATGGCATTA 327

QY 181 TCTTCCGCGGGAGATTCCAGGCAATGAGATGATATCCACTTACCTTTTCAAAATGA 240
Db 328 TCTTCCGCGGGAGATTCCAGGCAATGAGATGATATCCACTTACCTTTTCAAAATGA 387

QY 241 GACCTTGAAGAGACAGACCATATTATGCTGAAGCTGGCTGCAAGATGCTGTATC 300
Db 388 GACCTTGAAGAGAGACAGACCATATTATGCTGAAGCTGGCTGCAAGATGCTGTATC 447

QY 301 TGACCAAGCTCCCTTCTGATTTCACTACTATGCGAAGTGGCAAAATGATCTTTGGAG 360
Db 448 TGACCAAGCTCCCTTCTGATTTCACTACTATGCGAAGTGGCAAAATGATCTTTGGAG 507

QY 361 ATTTCAGTGTAGTTATCCGCTTCAAGCTTCCATTCACCTGTATAGAGCACTCCCT 420
Db 508 ATTTCAGTGTAGTTATCCGCTTCAAGCTTCCATTCACCTGTATAGAGCACTCCCT 567

QY 421 TCTCACTGTTTCAGCATCTTCGCTACTAGTGTATCATTCACCCATAGAGCTGCTTT 480
Db 568 TCTCACTGTTTCAGCATCTTCGCTACTAGTGTATCATTCACCCATAGAGCTGCTTT 627

QY 481 CCATTCAAAACTCGATGTGAGTTGAGCTGTGCTGTGTGTGTGATCATTTCACTGG 540
Db 628 CCATTCAAAACTCGATGTGAGTTGAGCTGTGCTGTGTGTGTGATCATTTCACTGG 687

QY 541 TAGCTGTCAATCCGATGACCTTCTTATCATATCAACCAAGACCAAGATCAAGCT 600
Db 688 TAGCTGTCAATCCGATGACCTTCTTATCATATCAACCAAGACCAAGATCAAGCT 747

QY 601 GTCTGACCTCAGAGTGGATGAACTCAATATATTAAGTGTAAACCTGTATTTGA 660
Db 748 GTCTGACCTCAGAGTGGATGAACTCAATATATTAAGTGTAAACCTGTATTTGA 807

QY 661 CTGCAACTATTTCTGCTCCCTTGTGTATGATGACATTTGTATACCAAGATATTC 720
Db 808 CTGCAACTATTTCTGCTCCCTTGTGTATGATGACATTTGTATACCAAGATATTC 867

QY 721 ACACTGTACCCATGTGCAAACTGACAGCTGCTTAAGCAGAAAAGCAAGAGCTAA 780
Db 868 ACACTGTACCCATGTGCAAACTGACAGCTGCTTAAGCAGAAAAGCAAGAGCTAA 927

QY 781 CCATTCTGCTACTCTCTTGCAATTTTACGTATGTTTTTACCCTTCATATCTTGAAGGTCA 840

/codon_start=-1
/evidence=not experimental
/product="seven transmembrane helix receptor"
/protein_id="BAC06095.1"
/db_xref="GI:21929019"
/translation="MNEPDLVLANSDPFDYAAFGNCTDENIPLKHYLPVYGIIF
LVGPENAVVISTYIFRMKPKSSTIMMIACTDLYLPLHYVSGEMWIFG
DMWCKIRSFENLYSILFLPCPSIFRVLHPSGSIHTRCAVAVAVWII
SLVAVIPMFELTSTNRNNSACLDLSDSELMITKYNILIRATPECLPIVITLCY
TTIHTLHGLDIOISCKOKARBLTILLALFVCPPLPHILVIRIRESLTLISCSI
ENQIHAYIVSRPLALNLTGNLILYVSDNFQAVGSTRCKVSNLEQAKKISTIS
NNP"
BASE COUNT      376 a      337 c      260 g      441 t
ORIGIN
Query Match      100.0%; Score 1081; DB 9; Length 1414;
Best Local Similarity 100.0%; Pred. No. 9,3e-271;
Matches 1081; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATATTGCCAACTGAAGTCTCTGTTTCTTGCAAGATGAAGAGCAACATGAATG 60
Db 148 CATATTGCCAACTGAAGTCTCTGTTTCTTGCAAGATGAAGAGCAACATGAATG 207

QY 61 AGCCACTAGACTATTAGCAATGCTTCTGATTTCCCGATTATGACGCTCTTTGGAA 120
Db 208 AGCCACTAGACTATTAGCAATGCTTCTGATTTCCCGATTATGACGCTCTTTGGAA 267

QY 121 ATTGCACTGATGAAACATGCCACTCAAGATGCACTACCTCCCTGTTATTTATGGCATTA 180
Db 268 ATTGCACTGATGAAACATGCCACTCAAGATGCACTACCTCCCTGTTATTTATGGCATTA 327

QY 181 TCTTCCGCGGGAGATTCCAGGCAATGAGATGATATCCACTTACCTTTTCAAAATGA 240
Db 328 TCTTCCGCGGGAGATTCCAGGCAATGAGATGATATCCACTTACCTTTTCAAAATGA 387

QY 241 GACCTTGAAGAGACAGACCATATTATGCTGAAGCTGGCTGCAAGATGCTGTATC 300
Db 388 GACCTTGAAGAGAGACAGACCATATTATGCTGAAGCTGGCTGCAAGATGCTGTATC 447

QY 301 TGACCAAGCTCCCTTCTGATTTCACTACTATGCGAAGTGGCAAAATGATCTTTGGAG 360
Db 448 TGACCAAGCTCCCTTCTGATTTCACTACTATGCGAAGTGGCAAAATGATCTTTGGAG 507

QY 361 ATTTCAGTGTAGTTATCCGCTTCAAGCTTCCATTCACCTGTATAGAGCACTCCCT 420
Db 508 ATTTCAGTGTAGTTATCCGCTTCAAGCTTCCATTCACCTGTATAGAGCACTCCCT 567

QY 421 TCTCACTGTTTCAGCATCTTCGCTACTAGTGTATCATTCACCCATAGAGCTGCTTT 480
Db 568 TCTCACTGTTTCAGCATCTTCGCTACTAGTGTATCATTCACCCATAGAGCTGCTTT 627

QY 481 CCATTCAAAACTCGATGTGAGTTGAGCTGTGCTGTGTGTGTGATCATTTCACTGG 540
Db 628 CCATTCAAAACTCGATGTGAGTTGAGCTGTGCTGTGTGTGTGATCATTTCACTGG 687

QY 541 TAGCTGTCAATCCGATGACCTTCTTATCATATCAACCAAGACCAAGATCAAGCT 600
Db 688 TAGCTGTCAATCCGATGACCTTCTTATCATATCAACCAAGACCAAGATCAAGCT 747

QY 601 GTCTGACCTCAGAGTGGATGAACTCAATATATTAAGTGTAAACCTGTATTTGA 660
Db 748 GTCTGACCTCAGAGTGGATGAACTCAATATATTAAGTGTAAACCTGTATTTGA 807

QY 661 CTGCAACTATTTCTGCTCCCTTGTGTATGATGACATTTGTATACCAAGATATTC 720
Db 808 CTGCAACTATTTCTGCTCCCTTGTGTATGATGACATTTGTATACCAAGATATTC 867

QY 721 ACACTGTACCCATGTGCAAACTGACAGCTGCTTAAGCAGAAAAGCAAGAGCTAA 780
Db 868 ACACTGTACCCATGTGCAAACTGACAGCTGCTTAAGCAGAAAAGCAAGAGCTAA 927

QY 781 CCATTCTGCTACTCTCTTGCAATTTTACGTATGTTTTTACCCTTCATATCTTGAAGGTCA 840

/codon_start=-1
/evidence=not experimental
/product="seven transmembrane helix receptor"
/protein_id="BAC06095.1"
/db_xref="GI:21929019"
/translation="MNEPDLVLANSDPFDYAAFGNCTDENIPLKHYLPVYGIIF
LVGPENAVVISTYIFRMKPKSSTIMMIACTDLYLPLHYVSGEMWIFG
DMWCKIRSFENLYSILFLPCPSIFRVLHPSGSIHTRCAVAVAVWII
SLVAVIPMFELTSTNRNNSACLDLSDSELMITKYNILIRATPECLPIVITLCY
TTIHTLHGLDIOISCKOKARBLTILLALFVCPPLPHILVIRIRESLTLISCSI
ENQIHAYIVSRPLALNLTGNLILYVSDNFQAVGSTRCKVSNLEQAKKISTIS
NNP"
BASE COUNT      376 a      337 c      260 g      441 t
ORIGIN
Query Match      100.0%; Score 1081; DB 9; Length 1414;
Best Local Similarity 100.0%; Pred. No. 9,3e-271;
Matches 1081; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATATTGCCAACTGAAGTCTCTGTTTCTTGCAAGATGAAGAGCAACATGAATG 60
Db 148 CATATTGCCAACTGAAGTCTCTGTTTCTTGCAAGATGAAGAGCAACATGAATG 207

QY 61 AGCCACTAGACTATTAGCAATGCTTCTGATTTCCCGATTATGACGCTCTTTGGAA 120
Db 208 AGCCACTAGACTATTAGCAATGCTTCTGATTTCCCGATTATGACGCTCTTTGGAA 267

QY 121 ATTGCACTGATGAAACATGCCACTCAAGATGCACTACCTCCCTGTTATTTATGGCATTA 180
Db 268 ATTGCACTGATGAAACATGCCACTCAAGATGCACTACCTCCCTGTTATTTATGGCATTA 327

QY 181 TCTTCCGCGGGAGATTCCAGGCAATGAGATGATATCCACTTACCTTTTCAAAATGA 240
Db 328 TCTTCCGCGGGAGATTCCAGGCAATGAGATGATATCCACTTACCTTTTCAAAATGA 387

QY 241 GACCTTGAAGAGACAGACCATATTATGCTGAAGCTGGCTGCAAGATGCTGTATC 300
Db 388 GACCTTGAAGAGAGACAGACCATATTATGCTGAAGCTGGCTGCAAGATGCTGTATC 447

QY 301 TGACCAAGCTCCCTTCTGATTTCACTACTATGCGAAGTGGCAAAATGATCTTTGGAG 360
Db 448 TGACCAAGCTCCCTTCTGATTTCACTACTATGCGAAGTGGCAAAATGATCTTTGGAG 507

QY 361 ATTTCAGTGTAGTTATCCGCTTCAAGCTTCCATTCACCTGTATAGAGCACTCCCT 420
Db 508 ATTTCAGTGTAGTTATCCGCTTCAAGCTTCCATTCACCTGTATAGAGCACTCCCT 567

QY 421 TCTCACTGTTTCAGCATCTTCGCTACTAGTGTATCATTCACCCATAGAGCTGCTTT 480
Db 568 TCTCACTGTTTCAGCATCTTCGCTACTAGTGTATCATTCACCCATAGAGCTGCTTT 627

QY 481 CCATTCAAAACTCGATGTGAGTTGAGCTGTGCTGTGTGTGTGATCATTTCACTGG 540
Db 628 CCATTCAAAACTCGATGTGAGTTGAGCTGTGCTGTGTGTGTGATCATTTCACTGG 687

QY 541 TAGCTGTCAATCCGATGACCTTCTTATCATATCAACCAAGACCAAGATCAAGCT 600
Db 688 TAGCTGTCAATCCGATGACCTTCTTATCATATCAACCAAGACCAAGATCAAGCT 747

QY 601 GTCTGACCTCAGAGTGGATGAACTCAATATATTAAGTGTAAACCTGTATTTGA 660
Db 748 GTCTGACCTCAGAGTGGATGAACTCAATATATTAAGTGTAAACCTGTATTTGA 807

QY 661 CTGCAACTATTTCTGCTCCCTTGTGTATGATGACATTTGTATACCAAGATATTC 720
Db 808 CTGCAACTATTTCTGCTCCCTTGTGTATGATGACATTTGTATACCAAGATATTC 867

QY 721 ACACTGTACCCATGTGCAAACTGACAGCTGCTTAAGCAGAAAAGCAAGAGCTAA 780
Db 868 ACACTGTACCCATGTGCAAACTGACAGCTGCTTAAGCAGAAAAGCAAGAGCTAA 927

QY 781 CCATTCTGCTACTCTCTTGCAATTTTACGTATGTTTTTACCCTTCATATCTTGAAGGTCA 840

```

Db 4844 TAGACAGCCCTCCCTTCCTGATTCACACATGACAGTGGGAGAAACCTGGATCTTTGGAG 4785

Qy 361 ATTTCATGCTGTAAGTTTATCCGCTTCAGCTTCATTTCAAACCTGTATAGCAGATCCCTCT 420

Db 4784 ATTTCATGCTGTAAGTTTATCCGCTTCAGCTTCATTTCAAACCTGTATAGCAGATCCCTCT 4725

Qy 421 TCCCTCAGCTGTTACAGATCTTCGCGATCGTGTGATCATTTCAACCAATGAGCTGCTTTT 480

Db 4724 TCCCTCAGCTGTTACAGATCTTCGCGATCGTGTGATCATTTCAACCAATGAGCTGCTTTT 4665

Qy 481 CCATTCACAAAACCTCGATGTGACGTTGTAGCCTGTGCTGTGAGTGTGATCATTTCACTGG 540

Db 4664 CCATTCACAAAACCTCGATGTGACGTTGTAGCCTGTGCTGTGAGTGTGATCATTTCACTGG 4605

Qy 541 TAGCTGTCAATCCGATGACCTTTTGTATCATATCAACCAACAGACCAACAGATCAAGCTT 600

Db 4604 TAGCTGTCAATCCGATGACCTTTTGTATCATATCAACCAACAGACCAACAGATCAAGCTT 4545

Qy 601 GTCTGACCTCACAGATGCGGATGGAATCTCAATCTATTAAGTGTATCAACCTGATTTTGA 660

Db 4544 GTCTGACCTCACAGATGCGGATGGAATCTCAATCTATTAAGTGTATCAACCTGATTTTGA 4485

Qy 661 CTGCACTACTTCTCTGCTCCCTCTGAGTGTATGTGACACTTGTCTTAAACAGATTAATCC 720

Db 4484 CTGCACTACTTCTCTGCTCCCTCTGAGTGTATGTGACACTTGTCTTAAACAGATTAATCC 4425

Qy 721 ACACTCTGACCCATGAGACTGCAACTGACAGCTGCTTAAAGCAAGAACGACGACGCTAA 780

Db 4424 ACACTCTGACCCATGAGACTGCAACTGACAGCTGCTTAAAGCAAGAACGACGACGCTAA 4365

Qy 781 CCATTCGTGTAACCTCTTGTGATTTTATGATGTTTATTTTACCCTTCATATCTTGAAGGTCA 840

Db 4364 CCATTCGTGTAACCTCTTGTGATTTTATGATGTTTATTTTATTTTATCCCTTCATATCTTGAAGGTCA 4305

Qy 841 TTCCGATCGAATCTGCGCTGCTTCAATGATGTTTCAATGAGATTCAGATTCATGAAG 900

Db 4304 TTCCGATCGAATCTGCGCTGCTTCAATGATGTTTCAATGAGATTCAGATTCATGAAG 4245

Qy 901 CTTAACGTGTTCTAGACCATTAAGCTGCTCTGAAACCTTTGGTAACTGTTACTATATAG 960

Db 4244 CTTAACGTGTTCTAGACCATTAAGCTGCTCTGAAACCTTTGGTAACTGTTACTATATAG 4185

Qy 961 TGGTGTGACGACCACTTTCAGACAGGCTGTCTGCTCAACAGTGAATGCAAGTAAGCG 1020

Db 4184 TGGTGTGACGACCACTTTCAGACAGGCTGTCTGCTCAACAGTGAATGCAAGTAAGCG 4125

Qy 1021 GGACCTTGAGACGACGAAAGAAATTAAGTATCTCAACCAACCTTGAATATTTCACTTA 1080

Db 4124 GGACCTTGAGACGACGAAAGAAATTAAGTATCTCAACCAACCTTGAATATTTCACTTA 4065

Qy 1081 C 1081

Db 4064 C 4064

RESULT 5  
LOCUS AC026756  
DEFINITION Homo sapiens chromosome 13 clone RP11-286P8, complete sequence.  
ACCESSION AC026756  
VERSION AC026756.15 GI:13112251  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 15655)  
Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D.,  
Federici,J., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R.,  
Mao,J., Lam,B., Marathe,R., Miranda,M., Morehouse,A.T., Nguyen,M.,  
Oefner,P., Palm,C.D., Ramirez,D., Southwick,A.M., Wilhelmy,J.,  
Yu,S. and Davis,R.W.

JOURNAL  
Unpublished

REFERENCE	AUTHORS	TITLE	JOURNAL
2 (bases 1 to 156555)	Abola, A.P., Bruno, D., Conn, L., Dela Rosa, M., Faulkner, D., Federgruel, N., Glukhov, S., Hansen, N., Herman, Z.S., Hyman, R., Mao, J., Marathe, R., Morehouse, A.J., Oefner, P., Palm, C.J., Ramirez, D., Wilhelmy, J., Yu, S. and Davis, R.W.	Submitted (23-MAR-2001) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA	
3 (bases 1 to 156555)	Abola, A.P., Bruno, D., Conn, L., Dela Rosa, M., Faulkner, D., Federgruel, N., Glukhov, S., Hansen, N., Herman, Z.S., Hyman, R., Lam, B., Mao, J., Marathe, R., Miranda, M., Morehouse, A.J., Nguyen, M., Oefner, P., Palm, C.J., Ramirez, D., Southwick, A.W., Wilhelmy, J., Yu, S. and Davis, R.W.	Submitted (23-FEB-2001) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA	
On Feb 23, 2001 this sequence version replaced gi:12745089.			
COMMENT			
Center: Stanford DNA Sequencing and Technology Development Center			
Center code: SPSMDC			
Web site: <a href="http://sequence-www.stanford.edu/group/human/">http://sequence-www.stanford.edu/group/human/</a>			
Contact: <a href="mailto:hum-info@sequence.stanford.edu">hum-info@sequence.stanford.edu</a>			
Project Information			
Center project name: 870			
Center clone name: RP11-286P8			
FEATURES			
Source			
Location/Qualifiers			
1..156555			
/organism="Homo sapiens"			
/db_xref="taxon:9606"			
/chromosome="13"			
/clone="RP11-286P8"			
/clone_11b="RBC1 human BAC library 11"			
BASE COUNT			
48748 a 30845 c 30755 g 46207 t			
ORIGIN			
Query Match	100.0%;	Score 1081;	DB 9; Length 156555;
Best Local Similarity	100.0%;	Pred. No. 1e-270;	
Matches 1081; Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;
1	CATATGGCAACGAACTCTCTGTTTCTTGGAAAGTGAAGAGCAACCATGATG	60	
Db 140135	CATATGGCAACGAACTCTCTGTTTCTTGGAAAGTGAAGAGCAACCATGATG	140194	
61	AGCACTAGACTATTAGCAATGCTTCTGATTTCCCGATTATGACCTGTTTGGAA	120	
Db 140195	AGCACTAGACTATTAGCAATGCTTCTGATTTCCCGATTATGACCTGTTTGGAA	140254	
121	ATTGCACTAGTAAAAACATCCGACTCAAGATGACATCTCCCTGTTATTTATG	180	
Db 140255	ATTGCACTAGTAAAAACATCCGACTCAAGATGACATCTCCCTGTTATTTATG	140314	
181	TCTTCTCGTGGGATTTCCAGGCAATGAGAGATATCCACTTATTTTCAAAAAGA	240	
Db 140315	TCTTCTCGTGGGATTTCCAGGCAATGAGAGATATCCACTTATTTTCAAAAAGA	140374	
241	GACCTTGGAGAGAGACCATCATTTATGCTGAACCTGGCTGACAGATCTGCTGATC	300	
Db 140375	GACCTTGGAGAGAGACCATCATTTATGCTGAACCTGGCTGACAGATCTGCTGATC	140434	
301	TGACAGACCTCCCTTCCTGATTCACATAATGCAAGTGGCGAAATGATCTTTGGAG	360	

Db 961 ACACTGTACCCATGATGCAAACTGACAGCTGCTTAAAGCAAGAAAGCAAGAGCTAA 1020

Qy 781 CCATTCGTACTCTCTGATTTTAAAGTATTTTAACTTCAATATCTGAGGCTCA 840

Db 1021 CCATTCGTACTCTCTGATTTTAAAGTATTTTAACTTCAATATCTGAGGCTCA 1080

Qy 841 TTGGATGCAATCTGCGCTCTTCAATCAATGTTTCATTTGAGAAATCAGATCCATGAG 900

Db 1081 TTGGATGCAATCTGCGCTCTTCAATCAATGTTTCATTTGAGAAATCAGATCCATGAG 1140

Qy 901 CTTAATGCTTTCTAGACCAATTAGCTGCTGTAACACCTTTGTAACCTGTTAATAAG 960

Db 1141 CTTAATGCTTTCTAGACCAATTAGCTGCTGTAACACCTTTGTAACCTGTTAATAAG 1200

Qy 961 TGGGTGATGAGCAACCTTTCAGCAGGCTGCTGCTCAACAGTGAATGAAATGAGG 1020

Db 1201 TGGGTGATGAGCAACCTTTCAGCAGGCTGCTGCTCAACAGTGAATGAAATGAGG 1260

Qy 1021 GGAACCTTGAGCAAGCAAAATTAAGTACTCAACAAACCTTGAATATTTGATTTA 1080

Db 1261 GGAACCTTGAGCAAGCAAAATTAAGTACTCAACAAACCTTGAATATTTGATTTA 1320

Qy 1081 C 1081

Db 1321 C 1321

RESULT 7

AF370886 1092 bp mRNA linear PRI 11-JUL-2002

LOCUS Homo sapiens G protein-coupled receptor GPR99 (GPR99) mRNA, complete cds.

ACCESSION AF370886 GI:21728283

VERSION AF370886.1

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1092)

AUTHORS Wittenberger, T., Heilebrand, S., Munk, A., Kreienkamp, H.J., Schaller, H.C. and Hampe, W.

TITLE GPR99, a new G protein-coupled receptor belonging to a new subgroup of nucleotide receptors

JOURNAL BMC Genomics 3 (1), 17 (2002)

PUBMED 12098360

REFERENCE 2 (bases 1 to 1092)

AUTHORS Hampe, W.

TITLE Direct Submission

JOURNAL Submitted (17-APR-2001) Developmental Neurobiology, Zentrum fuer Molekulare Neurobiologie, Martinistr. Hamburg 20246, Germany

FEATURES

source

1..1092

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/tissue\_type="Placenta"

1..1092

/gene="GPR99"

19..1032

/gene="GPR99"

/codon\_start=1

/product="G protein-coupled receptor GPR99"

/protein\_id="AA076912.1"

/db\_xref="GI:21728284"

/translation="MNEPDLTANASDPDYAAAFNCTDENIDPKMNYLPVIGIIFLVPGNAVVISTYIFKRPKSTIIMLNACTDLYLSPILHYVSGEMINGDFMCKIRSFHPLVSSILFLCFISIFRYCVLIHPSCFISHTKCAVAVAVMII SLAVAPMTFLTSINRTNSACLDLTSDESLNTIKYNNILITATCLPLVITVLTCTIIHLTHGLQDTSCKOKARLTIILLALFYCPLPHILIRIRIESRLISCSIE ENOIHAEYIVSRPLAALNTFNGLLLYVAVSDNFOAVCSITVCKVSGNLBQAKKISYS NNP"

gene

CDS

BASE COUNT 290 a 279 c 198 g 325 t

ORIGIN

Query Match 96.8%; Score 1046; DB 9; Length 1092;

Best Local Similarity 100.0%; Pred. No. 1.2e-261;

Matches 1046; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 AGATGAAGAGAGCAACGATGATGAGGCACTGACTATTTTACCAATGCTTCTGATTC 95

Db 1 AGATGAAGAGAGCAACGATGATGAGGCACTGACTATTTTACCAATGCTTCTGATTC 60

Qy 96 CCCGATTAAGCAGCTCTTTGGAATTTGCACTGATGAAACCAATCCACTCAAGATGAC 155

Db 61 CCCGATTAAGCAGCTCTTTGGAATTTGCACTGATGAAACCAATCCACTCAAGATGAC 120

Qy 156 TACCTCCCTGTTATTTTATGCAATTAATCTTCTGAGGATTTTCAGGCAATGAGTAGT 215

Db 121 TACCTCCCTGTTATTTTATGCAATTAATCTTCTGAGGATTTTCAGGCAATGAGTAGT 180

Qy 216 ATATGCACTTACATTTTCAAAATGAGACCTTGAAGAAGCAGCAATCATTAATGCTGAA 275

Db 181 ATATGCACTTACATTTTCAAAATGAGACCTTGAAGAAGCAGCAATCATTAATGCTGAA 240

Qy 276 CTGGCTGCAAGATCTGCTGATCTGACAGAGCTCCCTGCTGATCACTATGCTGAC 335

Db 241 CTGGCTGCAAGATCTGCTGATCTGACAGAGCTCCCTGCTGATCACTATGCTGAC 300

Qy 336 AGTGGGAAACTGATCTTTGGAATTTCAATGATGATTTATCCGCTTACAGCTTCAT 395

Db 301 AGTGGGAAACTGATCTTTGGAATTTCAATGATGATTTATCCGCTTACAGCTTCAT 360

Qy 396 TTCAACCTGTATAGCAGATCTCTTCTGACCTGTTTCAAGCAATCTTCCGTAATGATG 455

Db 361 TTCAACCTGTATAGCAGATCTCTTCTGACCTGTTTCAAGCAATCTTCCGTAATGATG 420

Qy 456 ATCAATTCACCAATGAGCTTTTCCATTCGAAACCTGATGACATGACATGATGAGCTGT 515

Db 421 ATCAATTCACCAATGAGCTTTTCCATTCGAAACCTGATGACATGATGAGCTGT 480

Qy 516 GGTGTGTGTGATCAATTTCACTGTGATGCTGATTCGATGACCTTCTTGAATCAATCA 575

Db 481 GGTGTGTGTGATCAATTTCACTGTGATGCTGATTCGATGACCTTCTTGAATCAATCA 540

Qy 576 ACCAAGAGCAAGCAAGATCAGCTGCTGCTGACCTTCAAGCAATGAGTGAATCAATCT 635

Db 541 ACCAAGAGCAAGCAAGATCAGCTGCTGCTGACCTTCAAGCAATGAGTGAATCAATCT 600

Qy 636 ATTAAGTGTAAACCTGATTTTGAATCTGCAATCTTCTGCTCCCTTGTGATAGTG 695

Db 601 ATTAAGTGTAAACCTGATTTTGAATCTGCAATCTTCTGCTCCCTTGTGATAGTG 660

Qy 696 ACACTTGTATACAGCAATTAATCAACTGACCTGACCAATGAGTGAATCAAGCTGCTG 755

Db 661 ACACTTGTATACAGCAATTAATCAACTGACCTGACCAATGAGTGAATCAAGCTGCTG 720

Qy 756 CTTAAGCAAGAGCAAGGCTAATCAATCTGCTACTCTTGAATTTTACGATGTTT 815

Db 721 CTTAAGCAAGAGCAAGGCTAATCAATCTGCTACTCTTGAATTTTACGATGTTT 780

Qy 816 TTACCTTCAATCTTGAAGGTCATTCGATGCAATCTGCTGCTCTTCAATCAATGATGT 875

Db 781 TTACCTTCAATCTTGAAGGTCATTCGATGCAATCTGCTGCTCTTCAATCAATGATGT 840

Qy 876 TCCATGAGATCAATCAATGAGCTTCAATGCTTTTCAAGCAATGAGCTGCTGAAAC 935

Db 841 TCCATGAGATCAATCAATGAGCTTCAATGCTTTTCAAGCAATGAGCTGCTGAAAC 900

Qy 936 ACCTTGTAACTGTTAATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 995

Db 901 ACCTTGTAACTGTTAATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960

Qy 996 TCAACAGGATGCAAGATGAGGGAACCTTGAAGCAAGCAAGAAATTAATGATGCTCA 1055

Db 961 TCAACAGGATGCAAGATGAGGGAACCTTGAAGCAAGCAAGAAATTAATGATGCTCA 1020

BASE COUNT	258 a	263 c	189 g	304 t	ORIGIN
Query Match	93.8%	Score 1014	DB 6	Length 1014	
Best Local Similarity	100.0%	Pred. No. 2.7e-253			
Matches 1014	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
QY	54	ATGAAATGAGCACTAGACATATTTAGCAAAATGCTTCTGATTTTCCCGATTATGACGTGCT	113		
DB	1	ATGAAATGAGCACTAGACATATTTAGCAAAATGCTTCTGATTTTCCCGATTATGACGTGCT	60		
QY	114	TTTGGAAATTTGCACTGATGAAAAATCCCACTCAAGATGACATTAAGTCTCCCTGTATTTAT	173		
DB	61	TTTGGAAATTTGCACTGATGAAAAATCCCACTCAAGATGACATTAAGTCTCCCTGTATTTAT	120		
QY	174	GGCATTAATCTTCTCGTGGGATTTTCCAGGCAATGAGTAGATATATCCATTAATTTTC	233		
DB	121	GGCATTAATCTTCTCGTGGGATTTTCCAGGCAATGAGTAGATATATCCATTAATTTTC	180		
QY	234	AAATATGAGACTTTGGAAGAGCAGCAACATCATTAATGCTGAACCTGGCTGCAAGATCTG	293		
DB	181	AAATATGAGACTTTGGAAGAGCAGCAACATCATTAATGCTGAACCTGGCTGCAAGATCTG	240		
QY	294	CTGTATCTGACAGAGCTCCCTCCGTGATTCCTATATGCAATGCAAGTGGGAAAACTGATC	353		
DB	241	CTGTATCTGACAGAGCTCCCTCCGTGATTCCTATATGCAATGCAAGTGGGAAAACTGATC	300		
QY	354	TTTGGAGATTTGATGTGTATGTTATTCGAGCTTCAAGCTTCAATTCAGCTGTATGAGC	413		
DB	301	TTTGGAGATTTGATGTGTATGTTATTCGAGCTTCAAGCTTCAATTCAGCTGTATGAGC	360		
QY	414	ATCTCTTCTCTCACTGTTTACAGATCTTCCGCTACTGTGATCATTTCAACCAATGAGC	473		
DB	361	ATCTCTTCTCTCACTGTTTACAGATCTTCCGCTACTGTGATCATTTCAACCAATGAGC	420		
QY	474	TGCTTTTTCATTCACAAAAATCGATGTCAGTTGATGAGCTGTGCTGTGTGTGATCATTT	533		
DB	421	TGCTTTTTCATTCACAAAAATCGATGTCAGTTGATGAGCTGTGCTGTGTGTGATCATTT	480		
QY	534	TCACGTGATGCTGATTCCTGATGACCTTCTTGTATCATATCAACCAAGAGCAAGCA	593		
DB	481	TCACGTGATGCTGATTCCTGATGACCTTCTTGTATCATATCAACCAAGAGCAAGCA	540		
QY	594	TCAGCTGTCTGACCTTCAACGATTCGATGAACTCATATCTATTAAGTGTGACACCTG	653		
DB	541	TCAGCTGTCTGACCTTCAACGATTCGATGAACTCATATCTATTAAGTGTGACACCTG	600		
QY	654	ATTTTGATCTGCACTACTCTTTCGCTCCCTGTGATGATGACACTTGTCTATACAGC	713		
DB	601	ATTTTGATCTGCACTACTCTTTCGCTCCCTGTGATGATGACACTTGTCTATACAGC	660		
QY	714	ATTATTCACACCTGAGACCCATGAGCTGGAATGACAGCTGCTTAAAGCAAGAACGCA	773		
DB	661	ATTATTCACACCTGAGACCCATGAGCTGGAATGACAGCTGCTTAAAGCAAGAACGCA	720		
QY	774	AGGCTAACCATTTCTGCTACTCTTGTGATTTTACATGATTTTAAACCTTCAATATCTG	833		
DB	721	AGGCTAACCATTTCTGCTACTCTTGTGATTTTACATGATTTTAAACCTTCAATATCTG	780		
QY	834	AGGCTCATTCGAGATCGAATCTCGCTGCTTCAATGATGTTTCATATGAAATCAGATC	893		
DB	781	AGGCTCATTCGAGATCGAATCTCGCTGCTTCAATGATGTTTCATATGAAATCAGATC	840		
QY	894	CATGAAGCTTACATCGTTTCTAGACCATTAAGCTGCTCTGAAACCTTTGGTAACTGTTA	953		
DB	841	CATGAAGCTTACATCGTTTCTAGACCATTAAGCTGCTCTGAAACCTTTGGTAACTGTTA	900		
QY	954	CTATATGTGTGTGTGATCAGCGCAAACTTTACAGAGAGCTCTCTGTCACACATGAGATGCAAA	1013		
DB	901	CTATATGTGTGTGTGATCAGCGCAAACTTTACAGAGAGCTCTCTGTCACACATGAGATGCAAA	960		
QY	1014	GTAACGGGAGCACTTGAGCAAGCAAGAAATAGTTACTCAAAACAACCTTGA	1067		



Search completed: January 30, 2003, 10:36:21  
Job time : 3480 secs



OM nucleic - nucleic search, using sw model

(without alignments)  
9016.334 Million cell updates/sec

Title: US-10-010-568-1  
Perfect score: 1081  
Sequence: 1 catattgccaaactgaactc.....ccttgaatatatttcatttac 1081

Scoring table: IDENTITY\_NUC

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : N\_GeneSeq\_101002:4

1:	/SID2/gcgdata/genseq/genseqn-emb1/NA1980.DAT.*
2:	/SID2/gcgdata/genseq/genseqn-emb1/NA1981.DAT.*
3:	/SID2/gcgdata/genseq/genseqn-emb1/NA1982.DAT.*
4:	/SID2/gcgdata/genseq/genseqn-emb1/NA1983.DAT.*
5:	/SID2/gcgdata/genseq/genseqn-emb1/NA1984.DAT.*
6:	/SID2/gcgdata/genseq/genseqn-emb1/NA1985.DAT.*
7:	/SID2/gcgdata/genseq/genseqn-emb1/NA1986.DAT.*
8:	/SID2/gcgdata/genseq/genseqn-emb1/NA1987.DAT.*
9:	/SID2/gcgdata/genseq/genseqn-emb1/NA1988.DAT.*
10:	/SID2/gcgdata/genseq/genseqn-emb1/NA1989.DAT.*
11:	/SID2/gcgdata/genseq/genseqn-emb1/NA1990.DAT.*
12:	/SID2/gcgdata/genseq/genseqn-emb1/NA1991.DAT.*
13:	/SID2/gcgdata/genseq/genseqn-emb1/NA1992.DAT.*
14:	/SID2/gcgdata/genseq/genseqn-emb1/NA1993.DAT.*
15:	/SID2/gcgdata/genseq/genseqn-emb1/NA1994.DAT.*
16:	/SID2/gcgdata/genseq/genseqn-emb1/NA1995.DAT.*
17:	/SID2/gcgdata/genseq/genseqn-emb1/NA1996.DAT.*
18:	/SID2/gcgdata/genseq/genseqn-emb1/NA1997.DAT.*
19:	/SID2/gcgdata/genseq/genseqn-emb1/NA1998.DAT.*
20:	/SID2/gcgdata/genseq/genseqn-emb1/NA1999.DAT.*
21:	/SID2/gcgdata/genseq/genseqn-emb1/NA2000.DAT.*
22:	/SID2/gcgdata/genseq/genseqn-emb1/NA2001.DAT.*
23:	/SID2/gcgdata/genseq/genseqn-emb1/NA2002.DAT.*
24:	/SID2/gcgdata/genseq/genseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Query No.	Score	Match	length	DB	ID	Description
1	1081	100.0	5435	24	AB56198	Human P2Y1-11 encod
2	1081	100.0	9905	24	AK938124	Human purinergic-x
3	1079.4	99.9	129	22	AA508362	Human cDNA encodin
4	1079.4	99.9	1729	23	AB24026	Human prostate exp
5	1079.4	99.9	1729	23	AB25767	Human prostate exp
6	1079.4	99.9	1729	23	AB29909	Human prostate exp
7	1079.4	99.9	1729	23	AB30024	Human prostate exp
8	1045	96.7	1288	23	AB56197	Human P2Y1-11 encod
9	1014	93.8	1014	22	AA507948	Human cDNA encodin

10	1014	93.8	1014	24	AEN85630	Human P2Y <sub>1</sub> -like receptor
11	1014	93.8	1014	24	ABK1381	Human DNA encoding
12	1014	93.8	1014	24	AKS98823	Human purinergic-1
13	1012.4	93.7	1014	24	AAQ78847	Human G-protein coupled
14	1012.4	93.7	1014	24	AAD34278	Human AXOR89 (G-protein
15	1012.4	93.7	1014	24	AAD26370	Human G-protein coupled
16	1011	93.5	1011	24	AAH43942	Human G-protein coupled
17	980.8	90.7	1020	22	AAH5011	Human nGPR54 codon
18	831	76.9	831	22	AEN85629	Human nGPR54 codon
19	779.4	72.1	1313	22	AAKS5430	Human P2Y <sub>1</sub> -like receptor
20	603.2	55.8	740	23	ABV15662	Human polynucleotide
21	538.8	49.8	578	22	AAH50998	Human prostatic exp
22	479.8	44.4	545	22	ABA08326	Human nGPR54 codon
23	479.8	44.4	545	22	AAK53141	Human P2Y purinergic
24	426.2	39.4	539	23	ABV3127	Human polynucleotide
25	426.2	39.4	539	23	ABV43465	Human prostatic exp
26	385	35.6	2245	23	ABV45465	Human prostatic exp
27	384.4	35.6	478	23	ABK1380	Human P2Y <sub>1</sub> -like G
28	382.4	35.4	426	23	ABV15479	Human prostatic exp
29	382.4	35.4	426	23	ABV35271	Human prostatic exp
30	364.8	33.7	435	23	ABV06310	Human prostatic exp
31	338.2	31.3	442	23	ABV08973	Human prostatic exp
32	242	22.4	657	22	AAK30831	Human prostatic exp
33	151	14.0	6721	24	AAAS18600	Human CDNA encoding
34	150.2	13.9	6721	24	AAAS18599	Purinergic receptor
35	137.6	12.7	1428	18	AAAT75146	Human ATP receptor
36	131.2	12.1	1005	21	AAD01135	Human orphan G-protein
37	131.2	12.1	1005	21	AAA4036	Human G-protein coupled
38	131.2	12.1	1436	24	ABL90790	Human polynucleotide
39	131.2	12.1	1542	24	AAD24958	Human G-protein coupled
40	129	11.9	1385	21	AAAC81122	Human secreted protein
41	129	11.9	1996	18	AAAT71900	Human purinergic-1
42	126.6	11.7	1543	24	ABK12957	DNA sequence of mouse
43	126.2	11.7	8423	24	ABL13407	Human immune system
44	123	11.4	1429	16	AAAT73321	Human P2Y <sub>1</sub> receptor
45	107.8	10.0	1163	22	AAD04981	Human purinergic-1

## ALIGNMENTS

```

RESULT 1
ABL56198
ID      ABL56198 standard; DNA; 5435 BP

```

AC ABL56198;

DT 05-JUL-2002 (first entry)

Human P2Y1-1i encoding genomic sequence

KW Human; p2yl-11; chromosome 13; G protein-coupled; receptor  
KW gene therapy; thyroid; ds.

OS Homo sapiens.

FH	Key	Location/Qualifiers
FT	CDS	
		3188..4201

/product= "p2y1-like purine receptor

PN DE10046970-A1

PD 11-APR-2002.  
YY

PF 22-SEP-2000; 2000DE-1046970.  
XX

PR 22-SEP-2000; 2000DE-1046970.  
XX

PA (BRUE/) BRUESS M.  
PA (BOEN/) BOENSTEN " "

XX	Briggs M	Boonick H
PT		



DR P-PSDB; AA014027.

XX Novel isolated G-protein coupled receptor peptide useful for treating  
PT disorder characterised by absence of, in appropriate or unwanted  
PT expression of the receptor protein, and as immunogens to raise  
PT antibodies

PS Claim 23; Fig 3; 64dp; English.

XX The present specifically claimed human genomic DNA sequence (located on  
CC chromosome 13) encodes a putative G-protein coupled receptor  
CC (GPCR) of the invention. GPCRs constitute a major class of proteins  
CC responsible for signal transduction within a cell. Upon binding of a  
CC ligand to the extracellular portion of a GPCR, a signal is transduced  
CC resulting in a biological or physiological change within the cell. The  
CC GPCR proteins can be divided into five families, family 1 contains the  
CC purinergic GPCRs (e.g. the P2Y receptors). P2Y receptors are  
CC characterised by their selective responsiveness towards ATP and its  
CC analogues, some also respond to UTP. The invention comprises a human  
CC G-protein coupled receptor protein and encoding nucleic acids. The GPCR  
CC protein and nucleic acids of the invention are useful in the treatment  
CC of a disease or condition mediated by a human protease. The GPCR protein of  
CC the invention is useful for the development/identification of  
CC therapeutic proteins; assays designed to quantitatively determine levels  
CC of the protein in biological fluids; identifying compounds which modulate  
CC the activity of the GPCR, or the interaction of the GPCR and a molecule  
CC with which it normally interacts; and treating a disorder characterised  
CC by an absence of, or inappropriate expression of the GPCR protein. The  
CC GPCR nucleic acids of the invention are useful in: diagnostic assays to  
CC identify changes in the GPCR nucleic acid that lead to pathology;  
CC controlling GPCR expression; and in gene therapy to treat patients with  
CC aberrant GPCR gene expression. The GPCR nucleic acids can also be used in  
CC the production of transgenic animals.

XX Sequence 9905 BP; 2656 A; 2218 C; 2061 G; 2970 T; 0 other;

Query Match 100.0%; Score 1081; DB 24; Length 9905;  
Best Local Similarity 100.0%; Pred. No. 1.9e-306;

Matches 1081; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATATGCCAACTGAACTCTCTGTTTCTGCAAGATGAAGAGACAAACATGAATG 60  
DB 8256 CATATGCCAACTGAACTCTCTGTTTCTGCAAGATGAAGAGACAAACATGAATG 8315  
QY 61 AGCCACTAGACTATTAGCAATGCTTCTGATTTCCCGATTATGACGCTGTTTGGAA 120  
DB 8316 AGCCACTAGACTATTAGCAATGCTTCTGATTTCCCGATTATGACGCTGTTTGGAA 8375  
QY 121 ATTGCACTGATGAAGAAATCCCACTCAAGATGACACTACCTCCCTGTTATTTATGAGCATTA 180  
DB 8376 ATTGCACTGATGAAGAAATCCCACTCAAGATGACACTACCTCCCTGTTATTTATGAGCATTA 8435  
QY 181 TCTTCTCGTGGGATTTCCAGCAATGATGATGATATTCATCTTCAAAAAGA 240  
DB 8436 TCTTCTCGTGGGATTTCCAGCAATGATGATGATATTCATCTTCAAAAAGA 8495  
QY 241 GACCTTGAAGAGAGACACATCATTTATGCTGAACCTGCGTGCACAGATGCTGTATTC 300  
DB 8496 GACCTTGAAGAGAGACACATCATTTATGCTGAACCTGCGTGCACAGATGCTGTATTC 8555  
QY 301 TGACCAAGCTCCCTCTCTGATTCATCTATGCAAGTGGGAAATGATCTTTGGAG 360  
DB 8556 TGACCAAGCTCCCTCTCTGATTCATCTATGCAAGTGGGAAATGATCTTTGGAG 8615  
QY 361 ATTTCATGTAAGTTATTCGCTTCACTGCTTCACTTCACTGATATGAGCATCTCT 420  
DB 8616 ATTTCATGTAAGTTATTCGCTTCACTGCTTCACTTCACTGATATGAGCATCTCT 8675  
QY 421 TCCCTCACTGTTTCAAGACTTCCGCTACTGATGATCATTCACCAATGAGCTGCTTT 480  
DB 8676 TCCCTCACTGTTTCAAGACTTCCGCTACTGATGATCATTCACCAATGAGCTGCTTT 8735  
QY 481 CCATTCAAAACATCGATGTCAGTTGAGCTGTGCTGTGTGATCATTTCACTGCG 540

DB 8736 CCATTCAAAACATCGATGTCAGTTGAGCTGTGCTGTGTGATCATTTCACTGCG 8795  
QY 541 TAGCTGTCAATTCGATGACCTTCTTGTATCATCAACCAAGAGACCAACATGACCT 600  
DB 8736 TAGCTGTCAATTCGATGACCTTCTTGTATCATCAACCAAGAGACCAACATGACCT 8855  
QY 601 GTCCTGACCTCCAGCTTGGATGATGATCATCTATTTAAGTGTCAACCTGATTTTGA 660  
DB 8856 GTCCTGACCTCCAGCTTGGATGATGATCATCTATTTAAGTGTCAACCTGATTTTGA 8915  
QY 661 CTGCAACTACTTTCGCTCCCTGCGTGTATGATGACCTTGTATTCACAGATTTATTC 720  
DB 8916 CTGCAACTACTTTCGCTCCCTGCGTGTATGATGACCTTGTATTCACAGATTTATTC 8975  
QY 721 ACACTGTACCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
DB 8976 ACACTGTACCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 9035  
QY 781 CCATTCTGCTACCTCTGCTGCTTCAATGATGATGATGATGATGATGATGATGATGATGAT 840  
DB 9036 CCATTCTGCTACCTCTGCTGCTTCAATGATGATGATGATGATGATGATGATGATGATGAT 9095  
QY 841 TTGCGATGAATTCGCTGCTGCTTCAATGATGATGATGATGATGATGATGATGATGATGAT 900  
DB 9096 TTGCGATGAATTCGCTGCTGCTTCAATGATGATGATGATGATGATGATGATGATGATGAT 9155  
QY 901 CTATCATGTTTCTAGACATTAAGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 960  
DB 9156 CTATCATGTTTCTAGACATTAAGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 9215  
QY 961 TGTGTGAGGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAATGCAAGTGAAGG 1020  
DB 9216 TGTGTGAGGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAATGCAAGTGAAGG 9275  
QY 1021 GGAACCTTGAGACCAAGAAATTAAGTACTCAACACACCTTGAATATTTCAATTA 1080  
DB 9276 GGAACCTTGAGACCAAGAAATTAAGTACTCAACACACCTTGAATATTTCAATTA 9335  
QY 1081 C 1081  
DB 9336 C 9336

RESULT 3  
AAS08362  
ID AAS08362 standard; cDNA; 1729 BP.  
XX  
AC AAS08362;  
XX  
DT 26-SEP-2001 (first entry)  
XX  
DB Human cDNA encoding G-protein coupled receptor, GPCR 39404.  
XX  
XX Human; G-protein coupled receptor; GPCR: 39404; immunogen; antibody;  
KW Good pasture's syndrome; viral hepatitis; Alzheimer's disease; lymphoma;  
KW Heymann nephritis; Paget's disease; Crohn's disease; endometriosis;  
KW systemic lupus erythematosus; actinic keratosis; myocarditis;  
KW Kawasaki syndrome; Digeorge syndrome; peripheral B-cell neoplasm;  
KW inflammations; teratoma; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 294..1307  
FT /tag= a  
FT /product= "Protein 39404"  
XX  
PN MO200149847-A2.  
XX  
XX 12-JUL-2001.  
XX  
XX 22-DEC-2000; 2000MO-US35309.



Query Match	99.9%	Score 1079.4	DB 263	Length 1729
Best Local Similarity	99.9%	Pred. No. 2.3e-306		
Matches 1080	Conservative	0	Mismatches 1	Indels 0
				Gaps 0

Db	901	CTGCAACTACTCTTTCGCTGCTCCCTTGGTGTGATGATGACACTTTCGTATACCAAGATTATCC	960
Qy	721	ACACTCTGACCCATGAGACTGCAAACTGACAGCTGCTTTAAGCAGAAAGCAGAGGCTTA	780
Db	961	AACTCTGACCCATGAGACTGCAAACTGACAGCTGCTTTAAGCAGAAAGCAGAGGCTTA	1020
Qy	781	CAATCTGCTACTGCTCTGCAATTTTAAGTATGTTTTTAACCTTCATATCTTGAAGGTCA	840
Db	1021	CAATCTGCTACTGCTCTGCAATTTTAAGTATGTTTTTAACCTTCATATCTTGAAGGTCA	1080
Qy	841	TTGCGATCGAATCTCGCTGCTTTTCATCAGTTGTTTCATTGAGAAATCGATCCATGAAG	900
Db	1081	TTGCGATCGAATCTCGCTGCTTTTCATCAGTTGTTTCATTGAGAAATCGATCCATGAAG	1140
Qy	901	CTTACATGCTTTCTTAAGCACTTAGCTGCTGGAACAACCTTGGTAACTGTACTATATG	960
Db	1141	CTTACATGCTTTCTTAAGCACTTAGCTGCTGGAACAACCTTGGTAACTGTACTATATG	1200
Qy	961	TGGGTGTGAGGAGCAACTTTGACAGAGGCTGTCTGCTCAGACGTGAGATGCAAAAGTAAAGG	1020
Db	1201	TGGGTGTGAGGAGCAACTTTGACAGAGGCTGTCTGCTCAGACGTGAGATGCAAAAGTAAAGG	1260
Qy	1021	GGAACCTTGAGCAGCAAGAAATAATAGTACTCAACAACCTTGAATAATTTCAATTA	1080
Db	1261	GGAACCTTGAGCAGCAAGAAATAATAGTACTCAACAACCTTGAATAATTTCAATTA	1320
Qy	1081	C 1081	
Db	1321	C 1321	
RESULT 7			
ABV30024	ABV30024 standard; cDNA; 1729 BP.		
AC	ABV30024;		
AC	16-SEP-2002 (first entry)		
DT	Human prostate expression marker		
DE	Human prostate expression marker		
XX	Human prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;		
XX	pharmacogenomic marker; gene; ss.		
XX	Homo sapiens.		
OS	WO200106060-A2.		
PD	23-AUG-2001.		
XX	20-FEB-2001; 2001WO-US05171.		
XX	17-FEB-2000; 2000US-183319P.		
PR	16-MAR-2000; 2000US-189862P.		
PR	25-MAY-2000; 2000US-207454P.		
PR	09-JUN-2000; 2000US-211314P.		
PR	18-JUL-2000; 2000US-219007P.		
PR	13-DEC-2000; 2000US-255281P.		
PA	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.		
XX	Schlegel R, Endege WO, Monahan JE;		
XX	WPI; 2001-662795/76.		
PT	Novel isolated nucleic acid molecule associated with cancerous state of		
PT	prostate cells and correlating with presence of prostate cancer, useful		
PT	for detecting presence of prostate cancer, stage of prostate cancer		
XX	Claim 1; Page 6487-6488; 11750pp; English.		
PS	The invention relates to an isolated nucleic acid molecule (I) comprising		
CC	a nucleotide sequence given in Tables 1-9 (abv00010-abv00019) of		
CC	sequence listing.		

CC sequence is that of the P2Y11 encoding cDNA.

XX Sequence 1288 BP; 347 A; 318 C; 241 G; 382 T; 0 other;

SQ Query Match 96.7%; Score 1045; DB 24; Length 1288;

Best Local Similarity 100.0%; Pred. No. 2,6e-296;

Matches 1045; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 37 GATGAAAGAGACACACATGATGAGCCATGATATTTGCAATGCTTCTGATTTCC 96
DB 1 GATGAAAGAGACACACATGATGAGCCATGATATTTGCAATGCTTCTGATTTCC 60
QY 97 CCGATTATGACGCTGCTTTGAAATGCACTGATGAAACATCCCACTCAAGATGACT 156
DB 61 CCGATTATGACGCTGCTTTGAAATGCACTGATGAAACATCCCACTCAAGATGACT 120
QY 157 ACCCTCCGTTATTTAATGAGCATTTCTCTGCGGATTTCCAGGCAATGAGTAGTGA 216
DB 121 ACCCTCCGTTATTTAATGAGCATTTCTCTGCGGATTTCCAGGCAATGAGTAGTGA 180
QY 217 TATCCACTTACATTTTCAAAATGAGACCTTGGAAAGAGACCATCTATATGCTGAAC 276
DB 181 TATCCACTTACATTTTCAAAATGAGACCTTGGAAAGAGACCATCTATATGCTGAAC 240
QY 277 TGGCTGACACAGATCTGCTGATCTGACAGCTCCCTCTGATTCATCTACTATGCGCA 336
DB 241 TGGCTGACACAGATCTGCTGATCTGACAGCTCCCTCTGATTCATCTACTATGCGCA 300
QY 337 GTGGCCGAAAAGCTGGATCTTTGAGAGATTTGATGTGATGATTCCTGCTTCACTTCAAT 396
DB 301 GTGGCCGAAAAGCTGGATCTTTGAGAGATTTGATGTGATGATTCCTGCTTCACTTCAAT 360
QY 397 TCAACCTGTATAGAGACATCTCTCCACCTGTTTCAAGATCTTCCGCTACTGTGTGA 456
DB 361 TCAACCTGTATAGAGACATCTCTCCACCTGTTTCAAGATCTTCCGCTACTGTGTGA 420
QY 457 TCAATTCACCCATGAGCTGCTTTTCCATTCACAAACCTGAGTGTAGCTGTG 516
DB 421 TCAATTCACCCATGAGCTGCTTTTCCATTCACAAACCTGAGTGTAGCTGTG 480
QY 517 CTGTGTGTGATGATTCATCTGCTGATCTGTGATTCGATGACCTTCTTGAATCAATCA 576
DB 481 CTGTGTGTGATGATTCATCTGCTGATCTGTGATTCGATGACCTTCTTGAATCAATCA 540
QY 577 CCAAGAGGACCAACATGATGAGCTGTCTGACCTTCAACAGTTTGGATGAATCAATCA 636
DB 541 CCAAGAGGACCAACATGATGAGCTGTCTGACCTTCAACAGTTTGGATGAATCAATCA 600
QY 637 TTAAGTGTACACATGATTTTGAAGTGAATCTTCTGCTCCCTGCTGTGTATGTA 696
DB 601 TTAAGTGTACACATGATTTTGAAGTGAATCTTCTGCTCCCTGCTGTGTATGTA 660
QY 697 CACTTGTCTATACAGATATTCACACTCTGACCCATGAGTGAAGTGAAGTGAAGTGC 756
DB 661 CACTTGTCTATACAGATATTCACACTCTGACCCATGAGTGAAGTGAAGTGAAGTGC 720
QY 757 TTAAGAGAAAGACAGAGGCTTACCATTTCTGCTACTCTTGTGATTTTACGATGTTTT 816
DB 721 TTAAGAGAAAGACAGAGGCTTACCATTTCTGCTACTCTTGTGATTTTACGATGTTTT 780
QY 817 TACCTTCATATCTTGAAGGTCATTCGATTCGAATTCGCTGCTTCAATGATTTT 876
DB 781 TACCTTCATATCTTGAAGGTCATTCGATTCGAATTCGCTGCTTCAATGATTTT 840
QY 877 CCATTGAGATCAGATTCATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 936
DB 841 CCATTGAGATCAGATTCATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 900
QY 937 CCTTGTGTAACCTGTTACTATATGTGTGTGACGACCACTTTCAGCAGGCTGTCTGCT 996
DB 901 CCTTGTGTAACCTGTTACTATATGTGTGTGACGACCACTTTCAGCAGGCTGTCTGCT 960
QY 997 CAACAGTGAATGACAAAGTAAGCGGAACTTGAAGCAAGCAAAATAATGTTACTCAA 1056

```

```

DB 961 CAACAGTGAATGACAAAGTAAGCGGAACTTGAAGCAAGCAAAATAATGTTACTCAA 1020
QY 1057 ACAACCTTGAATATTTCAATTAC 1081
DB 1021 ACAACCTTGAATATTTCAATTAC 1045

RESULT 9
AAS07948
ID AAS07948 standard; cDNA; 1014 BP.
XX
AC AAS07948;
XX
DT 23-OCT-2001 (first entry)
XX
DE Human cDNA encoding G-protein coupled receptor, hRUP21.
XX
KW Human; G-protein coupled receptor; GPCR; hRUP21; agonist;
KW Inverse agonist; lung cancer; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1014
FT /tag= a
FT /product= "hRUP21"

WO200136471-A2.
PD 25-MAY-2001.
XX
XX 16-NOV-2000; 2000WO-US31509.
XX
XX 17-NOV-1999; 99US-0166088.
XX 17-NOV-1999; 99US-0166099.
XX 17-NOV-1999; 99US-0166369.
XX 23-DEC-1999; 99US-0171901.
XX 23-DEC-1999; 99US-0171901.
XX 23-DEC-1999; 99US-0171902.
XX 11-FEB-2000; 2000US-0181749.
XX 14-MAR-2000; 2000US-0189258.
XX 14-MAR-2000; 2000US-0189259.
XX 10-APR-2000; 2000US-0195898.
XX 10-APR-2000; 2000US-0195899.
XX 10-APR-2000; 2000US-0196078.
XX 28-APR-2000; 2000US-0200419.
XX 12-MAY-2000; 2000US-0203630.
XX 12-JUN-2000; 2000US-0210741.
XX 12-JUN-2000; 2000US-0210982.
XX 21-AUG-2000; 2000US-0226760.
XX 26-SEP-2000; 2000US-0235418.
XX 26-SEP-2000; 2000US-0235779.
XX 20-OCT-2000; 2000US-0242332.
XX 20-OCT-2000; 2000US-0242343.
XX
XX (AREN-) ARENA PHARM INC.
XX
PI Chen R, Dang HT, Lowitz KP,
XX
XX WPI; 2001-355616/37.
XX
XX P-PSDB; AAV04375.
XX
XX Endogenous and non-endogenous versions of human G-protein coupled
XX PT receptors for direct identification of candidate compounds as agonists,
XX PT inverse agonists or partial agonists for use as therapeutic agents -
XX PS
XX Claim 55; Page 113-114; 159pp; English.
XX
XX The sequence encodes a human G-protein coupled receptor (GPCR),
XX hRUP21. The endogenous and non-endogenous, constitutively activated
XX versions of human G-protein coupled receptors (GPCR), are useful for
XX direct identification of candidate compounds as receptor agonists.

```

CC of the invention.

XX Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 other;

Query Match 93.8%; Score 1014; DB 24; Length 1014;  
Best Local Similarity 100.0%; Pred. No. 2.9e-287;  
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 ATGATGAGGCACTAGACCTATTGAGCAAAATGCTCTGATTTCCCGGATTATGACGCTGCT 113  
DB 1 ATGATGAGGCACTAGACCTATTGAGCAAAATGCTCTGATTTCCCGGATTATGACGCTGCT 60  
QY 114 TTGGAATGCACTGATGAAACATCCACTCAAGATGACCTCCCTGTTATTTAT 173  
DB 61 TTGGAATGCACTGATGAAACATCCACTCAAGATGACCTCCCTGTTATTTAT 120  
QY 174 GGCAATATCTCTCGGGGATTTCCGAGCAATGCAATGATGATCACTTACATTTTC 233  
DB 121 GGCAATATCTCTCGGGGATTTCCGAGCAATGCAATGATGATGATCACTTACATTTTC 180  
QY 234 AAAATAGACCTTGGAAAGACAGACCATCATTAATGCTGAACCTGGGCTGACAGATCTG 293  
DB 181 AAAATAGACCTTGGAAAGACAGACCATCATTAATGCTGAACCTGGGCTGACAGATCTG 240  
QY 294 CTGATCTGACCAAGCTCCCTCTCTGATTCACCTATGCAAGTGGCAAACTGGATC 353  
DB 241 CTGATCTGACCAAGCTCCCTCTCTGATTCACCTATGCAAGTGGCAAACTGGATC 300  
QY 354 TTGGAAGATTTGATGATGATTTATCCGCTTCACTTCAATTTGATGAGC 413  
DB 301 TTGGAAGATTTGATGATGATTTATCCGCTTCACTTCAATTTGATGAGC 360  
QY 414 ATCTCTCTCTGACCTGTTGACGATCTTCCGCTTCACTTCAATTTGATGAGC 473  
DB 361 ATCTCTCTCTGACCTGTTGACGATCTTCCGCTTCACTTCAATTTGATGAGC 420  
QY 474 TGCCTTTCCATTCAAAAATCGATGATGATGATGATGATGATGATGATGATGATGATGAT 533  
DB 421 TGCCTTTCCATTCAAAAATCGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
QY 534 TCACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 593  
DB 481 TCACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540  
QY 594 TCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 653  
DB 541 TCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600  
QY 654 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 713  
DB 601 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
QY 714 ATATTCACACTGTGACCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 773  
DB 661 ATATTCACACTGTGACCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720  
QY 774 AGGCTAATCATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 833  
DB 721 AGGCTAATCATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
QY 834 AGGCTAATCATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 893  
DB 781 AGGCTAATCATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840  
QY 894 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 953  
DB 841 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
QY 954 CTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1013  
DB 901 CTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960  
QY 1014 GTAAAGCGGAACTTGAAGCAAGCAAAAGAAATTAATTAATCAACCTTTGA 1067

DB 961 GTAAAGCGGAACTTGAAGCAAGCAAAAGAAATTAATTAATCAACCTTTGA 1014

RESULT 11  
ABK11381  
ID ABK11381 standard; DNA; 1014 BP.

XX ABK11381;

DT 05-JUN-2002 (first entry)

DE Human DNA encoding P2Y1-like G protein-coupled receptor.

XX Human; ds; gene; P2Y1-like G protein-coupled receptor; GPCR;  
KW infection; pain; cancer; anorexia; bulimia; asthma; hypertension;  
KW central nervous system disease; acute heart failure; hypertension;  
KW urinary retention; osteoporosis; diabetes; angina pectoris;  
KW myocardial infarction; ulcer; inflammation; allergy; multiple sclerosis;  
KW benign prostatic hypertrophy; psychosis; neurological disorder;  
KW Parkinson's disease; anxiety; schizophrenia; manic depression; delirium;  
KW dementia; severe mental retardation; Huntington's disease;  
KW Tourette's syndrome.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 1..1014

FT /tag= a

FT /product= "P2Y1-like GPCR"

XX WO200214511-A2.

XX 21-FEB-2002.

XX 10-AUG-2001; 2001WO-EP09243.

XX 14-AUG-2000; 2000US-224989P.

XX (FARB ) BAYER AG.

XX Ramakrishnan S;

XX WPI; 2002-257607/30.

XX P-PSDB; AAT7600.

XX Novel human P2Y1-like G protein-coupled receptor polypeptide which can

XX be regulated for treating infection, pain, cancer, diabetes, anorexia,

XX asthma, hypertension, neurological disorder and dyskinesia

XX Claim 1; Fig 5; 118pp; English.

XX The invention relates to a purified human P2Y1-like G protein-coupled

XX receptor (GPCR) polypeptide and the nucleic acids encoding it

XX (including 5' and 3' sequences, promoters, fragments, variants, or a

XX sequence encoding a protein at least 50% identical to the GPCR).

XX Also included are an expression vector comprising the nucleic acid,

XX a host cell containing the vector and the identification of modulators of

XX the GPCR especially those that reduce the activity of the GPCR.

XX The nucleic acid is useful for detecting a polynucleotide encoding

XX the GPCR in a biological sample. The GPCR and nucleic acid are useful for

XX screening for agents that decrease the activity of the GPCR and

XX for modulators of the GPCR. The modulator or agent useful for modulating

XX the activity of P2Y1-like G protein-coupled receptor in a disease such as

XX bacterial, fungal, protozoan, and viral infection, pain, cancer,

XX anorexia, bulimia, asthma, central nervous system (CNS) disease, acute

XX heart failure, hypotension, hypertension, urinary retention,

XX osteoporosis, diabetes, angina pectoris, myocardial infarction, ulcer,

XX inflammation, allergy, multiple sclerosis, benign prostatic hypertrophy,

XX psychotic and neurological disorders, dyskinesia, HIV virus infection

XX (human immunodeficiency virus), CNS disorders such as Parkinson's

XX disease, anxiety, schizophrenia, manic depression, delirium, dementia,

XX Tourette's syndrome.

XX SQ Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 other;

Query Match 93.8%; Score 1014; DB 24; Length 1014;  
Best Local Similarity 100.0%; Pred. No. 2.9e-287;  
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

54 ATGATGAGGACCTAGACCTATTGACAAATGCTTCTGATTTCCCGATTATGACAGTGGT 113  
1 ATGAATGAGGACCTAGACCTATTGACAAATGCTTCTGATTTCCCGATTATGACAGTGGT 60  
114 TTGGAATGACCTGATGAAACATCCCACTCAAGATGACCTACCTCCGTATTATAT 173  
61 TTGGAATGACCTGATGAAACATCCCACTCAAGATGACCTACCTCCGTATTATAT 120  
174 GGCATTATCTCTCTGCGGATTTCCAGCAATGACAGATGATGATGATGATGATGAT 233  
121 GGCATTATCTCTCTGCGGATTTCCAGCAATGACAGATGATGATGATGATGATGATGAT 180  
234 AAAATGAGACCTTGGAAAGACAGACCATGATATGCTGAACTGGCTGACAGATCTG 293  
181 AAAATGAGACCTTGGAAAGACAGACCATGATATGCTGAACTGGCTGACAGATCTG 240  
294 CTGATCTGACCGCTCCCTCCCTCTGATTTCACTATGACAGTGGCAAACTGGATC 353  
241 CTGATCTGACCGCTCCCTCCCTCTGATTTCACTATGACAGTGGCAAACTGGATC 300  
354 TTGGAATGACCTGATGAAACATCCCACTCAAGATGACCTACCTCCGTATTATAT 413  
301 TTGGAATGACCTGATGAAACATCCCACTCAAGATGACCTACCTCCGTATTATAT 360  
414 ATCTCTTCTCTCACTGTTTCAAGACATCTTCCGCTACTGATGATGATGATGATGATGAT 473  
361 ATCTCTTCTCTCACTGTTTCAAGACATCTTCCGCTACTGATGATGATGATGATGATGAT 420  
474 TGCCTTTTCATTCACAAAACCTGATGATGATGATGATGATGATGATGATGATGATGAT 533  
421 TGCCTTTTCATTCACAAAACCTGATGATGATGATGATGATGATGATGATGATGATGAT 480  
534 TCACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 593  
481 TCACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540  
594 TCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 653  
541 TCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600  
654 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 713  
601 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
714 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 773  
661 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720  
774 AGGCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 833  
721 AGGCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
834 AGGCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 893  
781 AGGCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840  
894 CATAAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 953  
841 CATAAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
954 CATAAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1013  
901 CATAAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960  
1014 GTAAGCGGAACTTGAAGCAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1067

Db 961 GTAAGCGGAACTTGAAGCAAGAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1014

RESULT 13

AB078847  
ID AB078847 standard; cDNA; 1014 BP.

XX AB078847;

DT 04-OCT-2002 (first entry)

XX Human G-protein coupled receptor PFI-019 cDNA.

DE Human; G-protein coupled receptor; GPCR; PFI-019; neuroprotective;  
KW anti-inflammatory; cytosolic; cardiovascular; antiallergic; hypotensive;  
KW arteriosclerotic; osteopathic; hypertension; asthma;  
KW arteriosclerosis; gene; ss.

XX Homo sapiens.

OS Homo sapiens.  
FH Key Location/Qualifiers  
FT 1..1014  
FT CDS /tag= a  
FT /product= "PFI-019"

PN BP1219638-A2.

XX 03-JUL-2002.

PD 04-DEC-2001; 2001BP-0310136.

PF 18-DEC-2000; 2000GB-0030854.

PR 04-MAY-2001; 2001GB-0011031.

XX (PFI-019) PFIZER LTD.  
PA (PFI-019) PFIZER INC.

XX Fido MD;

PI WPI; 2002-521945/56.  
XX P-PSDB; ABB81902.

DR New G-protein coupled receptor (GPCR) polypeptide with homology to p2y

PT purinoreceptor, useful for treating e.g. inflammation or cancers in a

PT patient, or for screening GPCR agonists or antagonists for treating

PT these diseases

XX Claim 1; Page 12; 19p; English.

XX The invention relates to a novel G-protein coupled receptor (GPCR), and

CC the polynucleotide encoding it. The protein of the invention has

CC neuroprotective, anti-inflammatory, cytosolic, cardiovascular,

CC antiallergic, hypotensive, antiatherosclerotic, and osteopathic

CC activity. The GPCR polypeptide is useful for manufacturing a medicament

CC for treating a patient who needs to upregulate a receptor. Preferably,

CC therapeutically useful areas are hypertension, asthma, and

CC arteriosclerosis. The sequence encodes the G-protein coupled receptor

CC of the invention, PFI-019.

XX SQ Sequence 1014 BP; 259 A; 263 C; 188 G; 304 T; 0 other;

Query Match 93.7%; Score 1012.4; DB 24; Length 1014;  
Best Local Similarity 99.9%; Pred. No. 8.5e-287;  
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

54 ATGAATGAGCACTAGACCTATTGACAAATGCTTCTGATTTCCCGATTATGACAGTGGT 113  
1 ATGAATGAGCACTAGACCTATTGACAAATGCTTCTGATTTCCCGATTATGACAGTGGT 60  
114 TTGGAATGACCTGATGAAACATCCCACTCAAGATGACCTACCTCCGTATTATAT 173  
61 TTGGAATGACCTGATGAAACATCCCACTCAAGATGACCTACCTCCGTATTATAT 120





GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 06:48:56 : Search time 2177 Seconds

(without alignments)  
8041.948 Million cell updates/sec

Title: US-10-010-568-1  
Perfect score: 1081  
Sequence: 1 catattgccaactgaactc.....ccttgaatattcattac 1081

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

#### Database :

EST:  
1: em\_estba.\*  
2: em\_esthum.\*  
3: em\_estin.\*  
4: em\_estmu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_hcc.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_hcc.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: gb\_gss.\*  
18: em\_gss\_hum.\*  
19: em\_gss\_inv.\*  
20: em\_gss\_pln.\*  
21: em\_gss\_vrt.\*  
22: em\_gss\_fun.\*  
23: em\_gss\_mam.\*  
24: em\_gss\_mus.\*  
25: em\_gss\_other.\*  
26: em\_gss\_pro.\*  
27: em\_gss\_rtd.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	257	23.8	744	14	BM723768 UI-E-BOI-
2	126.6	11.7	623	14	BQ038875 pgnlc.pk0
3	115.6	10.7	641	14	BQ396255 NISC_ng19
4	114.6	10.6	638	9	AL675845 AL675845
5	109.4	10.1	877	12	BG402029 602466748
6	108.8	10.1	663	13	BM426517 pgfzn.pk0

Result No.	Score	Query Match	Length	DB ID	Description
7	107.4	9.9	1101	17	CNS05325
8	106.2	9.8	491	12	BG712193
9	103	9.5	609	9	AL588350
10	102	9.4	520	9	AL663305
11	100.4	9.3	2542	11	AK017378
12	100.4	9.3	3001	11	AK005013
13	100	9.3	422	10	BB847918
14	99.6	9.2	801	13	BQ924078
15	98.4	9.1	606	17	AZ953874
16	97.2	9.0	821	13	BI833118
17	96	8.9	639	10	BB660768
18	95.8	8.9	408	13	BI401676
19	95.8	8.9	1063	14	BM918491
20	94	8.7	420	10	BB864882
21	94	8.7	884	9	AL525099
22	94	8.7	898	13	BI819396
23	94	8.7	936	9	AL520218
24	93.8	8.7	484	14	BQ551383
25	93.8	8.7	523	9	AL836006
26	93.8	8.7	839	14	BQ897419
27	93.6	8.7	955	9	AL521440
28	93.4	8.6	934	13	BI768397
29	92.6	8.6	983	17	CNS048P5
30	92.4	8.5	899	14	BQ959110
31	91.6	8.5	678	10	BB314834
32	89.8	8.3	589	14	BQ396804
33	89.4	8.3	581	13	BM258063
34	87.6	8.1	734	13	BG914321
35	87.6	8.1	752	13	BM008116
36	87.6	8.1	801	13	BI837965
37	87.6	8.1	870	9	AL545172
38	87.6	8.1	885	9	AL546894
39	87.6	8.1	1057	14	BM918711
40	87.6	8.1	2146	11	BC027965
41	87.2	8.1	529	9	AA177828
42	87.2	8.1	585	10	BB827479
43	86.8	8.0	570	12	BG579061
44	86.8	8.0	869	14	BQ724793
45	86.8	8.0	1101	17	CNS044V3

#### ALIGNMENTS

RESULT 1  
BM723768  
DEFINITION  
UI-E-BOI-aix-g-16-0-UI-r1 UI-E-BOI Homo sapiens CDNA clone  
BM723768  
ACCESSION  
BM723768  
VERSION  
BM723768.1 GI:19045099  
SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 744)  
Bonaldo,M.F., Lemon,G. and Soares,M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
JOURNAL  
Genome Res. 6 (9), 791-806 (1996)  
MEDLINE  
97044477  
COMMENT  
Contact: Soares, MB  
Program for Rat Gene Discovery and Mapping  
University of Iowa  
451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: msotares@iuc.wieg.uiowa.edu  
Tissue Procurement: Dr. Gregg Hageman  
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. W. Bento Soares, University of Iowa

KEYWORDS EST.  
SOURCE western clawed frog.  
ORGANISM Silurana tropicalis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
Xenopodinae; Silurana.  
REFERENCE  
AUTHORS NIH-XGC [http://image.jnl.gov/image/html/xenopuslib\\_info.shtml](http://image.jnl.gov/image/html/xenopuslib_info.shtml).  
TITLE 1 (bases 1 to 641)  
JOURNAL NIH-XGC  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
CDNA Library Preparation:  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC)  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.jnl.gov>  
Plate: LLML1977 row: N column: 13  
Seq primer: M13RP1 reverse primer (ABI).  
Location/Qualifiers  
1..641  
/organism="Silurana tropicalis"  
/db\_xref="taxon:8364"  
/clone="IMAGE:538384"  
/clone\_lib="NICHD XGC Emb6"  
/tissue\_type="neural"  
/dev\_stage="embryo, stages 14-19"  
/lab\_host="pHD10B (phage-resistant)"  
/note="Vector: pCMV-SPORT6, ccdB. Site 1: NotI; Site 2:  
EcoRV; Cloned unidirectionally. Primer: Oligo dt. Average  
insert size 2.1 kb. Constructed by Invitrogen. Note: This  
is a Xenopus Gene Collection (XGC) library."

BASE COUNT 132 a 184 c 153 g 172 t  
ORIGIN

Query Match 10.7%; Score 115.6; DB 14; Length 641;  
Best Local Similarity 51.8%; Pred. No. 4,5e-22;  
Matches 262; Conservative 0; Mismatches 244; Indels 0; Gaps 0;

145 TCAAGATGACATCACTCCCTGTTATTATGAGCTATATCTTCCTCGGGATTTCCAGGCA 204  
125 TCAAGTACGTCCTCTCCCGGTGTCGACGACATCGTTCGCGGGGCTGATCTGA 184  
205 ATGAGTAGTATATCACTTACATTTTCAAAATGAGACCTTGAGAGAGACCATCA 264  
185 ACATTCGACCTGTACATCTTCTTCGATCAAGCCCTGGAAGCCTCCACACCT 244  
265 TTATGCTGAACCTGCGCTGACAGATCTGCTATCTGACAGCCTCCCTTCGATTG 324  
245 ACATTTCAACTGGGCATTTCCGACATGATGACATCTCCCTCCGCTGCTGCT 304  
325 ACTACTATGCGAGTGGCGAAAAGTGGATCTTTGAGATTTCAATGTATATCCGCT 384  
305 ATTACTACTCGGAGGGGCAACTGGCCGTGCGCTGCGCTTGCAAGATGTCAGG 364  
385 TCAGTTCCATTTCAACCTGTATAGAGACATCTCTTCCTCACTCTTTTCAAGATTTCC 444  
365 TCTTTTTCACCAACATGTAAGTATGATCTCTCTTCTGCTGTCATCAGATCACCC 424  
445 GCTACTGTGTATCATTTCAACCAATGAGCTGCTTTTTCATTCACAAATCTGATGCA 504  
425 GCTTCCTGGGATCTGCTACCAATGAAATCACTCGTTGGCTGGAAGTGGCAATGCTC 484  
505 TTGATGCTGTGCTGTGTGATCATTTCACTGTAGCTGTCAATTCGATGACCTTCT 564  
485 GGATATATTCCTGTGCTGTGTGATCATTTCCGCTGTGATGCTCCCTATATTTACT 544  
565 TGATCATCATCAACCAAGACCAAGATGAGCTGTGCTGACCTCCACAGTTGGAGT 624  
545 TTGTTACACCAAGTTCAATGGGAGACCACTGCGCATGACCTTCCAGGCTGATC 604

625 AACCTAATCTATTAAGTGATCAAC 650  
605 TATTTGACACTTTGTGCTTACGC 630

RESULT 4  
LOCUS AL675845  
DEFINITION AL675845 XGC-gastrula silurana tropicalis cDNA clone Tga051n19 5',  
mRNA sequence.  
ACCESSION AL675845  
VERSION AL675845.1 GI:19532219  
KEYWORDS EST.  
SOURCE western clawed frog.  
ORGANISM Silurana tropicalis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
Xenopodinae; Silurana.  
REFERENCE  
AUTHORS Taylor, R., Ashurst, J.L., Croning, M.D.R., Zorn, A.M. and Rogers, J.  
TITLE Sanger Xenopus tropicalis EST project 2002  
JOURNAL Unpublished (2001)  
COMMENT Contact: Taylor R  
Sanger Centre  
Hinxton, Cambridgeshire, CB10 1SA, UK  
Email: [trop@sanger.ac.uk](mailto:trop@sanger.ac.uk)  
Sanger Xenopus tropicalis EST project 2001  
TROPICALIS SEQUENCE ID: TGA051n19.p1csp6  
This sequence is from a Xenopus Gene Collection (XGC) library  
constructed by Aaron M. Zorn.

BASE COUNT 134 a 180 c 144 g 179 t 1 others  
ORIGIN

Query Match 10.6%; Score 114.6; DB 9; Length 638;  
Best Local Similarity 51.6%; Pred. No. 8,8e-22;  
Matches 261; Conservative 0; Mismatches 245; Indels 0; Gaps 0;

145 TCAAGATGACATCACTCCCTGTTATTATGAGCTATATCTTCCTCGGGATTTCCAGGCA 204  
121 TCAAGTACGTCCTCTCCCGGTGTCGACGACATCGTTCGCGGGGCTGATCTGA 180  
205 ATGAGTAGTATATCACTTACATTTTCAAAATGAGACCTTGAGAGAGACCATCA 264  
181 ACATTCGACCTGTACATCTTCTTCGATCAAGCCCTGGAAGCCTCCACACCT 240  
265 TTATGCTGAACCTGCGCTGACAGATCTGCTATCTGACAGCCTCCCTTCGATTG 324  
241 ACATGTTCAACCTGGCATTTCCGACATGATGACATCTCCCTCCGCTGCTGCT 300  
325 ACTACTATGCGAGTGGCGAAAAGTGGATCTTTGAGATTTCAATGTATATCCGCT 384  
301 ATTACTACTCGGAGGGGCAACTGGCCGTGCGCTGCGCTTGCAAGATGTCAGG 360  
385 TCAGTTCCATTTCAACCTGTATAGAGACATCTCTTCCTCACTCTTTTCAAGATTTCC 444  
361 TCTTTTTCACCAACATGTAAGTATGATCTCTCTTCTGCTGTCATCAGATCACCC 420  
445 GCTACTGTGTATCATTTCAACCAATGAGCTGCTTTTTCATTCACAAATCTGATGCA 504

Db 335 TCAGTTCTACTACCTGCCCCACCGTCTACATCTCTGTTTCATCACCGGGTCTTGGGCA 394  
 Qy 205 ATGAGTAGTAGTATTCACCTTATACATTTTGAAGAGACCTTGAAGAGACCATCA 264  
 Db 335 ACAGGTGGCCATCTGGAATTTGTTCTTCCACATGGCGCGTGAAGCGGATCTGGTGT 454  
 Qy 265 TTATGCTGAACCTGGCTGCAACAGATCTGCTATCTGACACAGCTCCCTCTGATTC 324  
 Db 455 ACATGTTCAACCTGGCTGCGGCACTTCTGTATGTCCACAGCTGCGGCCCTCATCT 514  
 Qy 325 ACTACTATGCGAGTGGCGGAAAAGTGAATCTTTGGAATTTGATGTGAATTTATCCGCT 384  
 Db 515 TCTACTACTTCAACAAACCGGACTGATCTTGGGAGACGTCATGTGCAAGCTGAGAGT 574  
 Qy 385 TCAGTTCCATTTCAACCTGTATAGAGACATCTCTTCTCCACCTGTTTATGACATCTCC 444  
 Db 575 TCATTTTCCACGTGAACCTCTAGGAGACATCTTNNCTCAGCTGATTAAGGATGNNCA 634  
 Qy 445 GCTACTGTGTGATTCATTCACCCATGA 471  
 Db 635 GGTATACGGCGCTCGTNNCCCGCTGA 661

RESULT 7  
 CDS05328/c 1101 bp DNA linear GSS 26-JUL-2000  
 LOCUS Tetraodon nigroviridis genome survey sequence IV end of clone  
 DEFINITION 020M21 of library A from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION ALJ18925.1 GI:9551809  
 VERSION GSS: genome survey sequence.  
 KEYWORDS Tetraodon nigroviridis.  
 SOURCE Tetraodon nigroviridis.  
 ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

REFERENCE 1 (bases 1 to 1101)  
 AUTHORS Reest Croillius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W., Saurin,W. and Weissenbach,J.  
 TITLE Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence  
 JOURNAL Nat. Genet. 25 (2), 235-238 (2000)  
 MEDLINE 20296633  
 PUBMED 10835645

REFERENCE 2 (bases 1 to 1101)  
 AUTHORS Croillius,H.R., Jallion,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.  
 TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis  
 JOURNAL Genome Res. 10 (7), 939-949 (2000)  
 MEDLINE 20359837  
 PUBMED 10899143

REFERENCE 3 (bases 1 to 1101)  
 AUTHORS Genoscope.  
 TITLE Direct Submission  
 JOURNAL Submitted (12-APR-2000)  
 COMMENT This sequence is a single read and was generated as part of a large scale clone-and-sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

## FEATURES

source  
 1..1101  
 /organism="Tetraodon nigroviridis"  
 /db\_xref="taxon:99883"  
 /clone="020M21"  
 /clone\_lib="A"  
 /note="Genoscope sequence ID : COAA020AG11C1-end : T7"

BASE COUNT 305 a 216 c 280 g 284 t 16 others  
 ORIGIN

Query Match 9 %; Score 107.4; DB 17; Length 1101;  
 Best Local Similarity 54.0%; Pred. No. 1,3e-19;  
 Matches 258; Conservative 0; Mismatches 216; Indels 4; Gaps 2;

Qy 145 TCAAGATGACACTCTCCCTGTTATTTATGAGATTTCTTCTCGTGGGATTTCCAGGCA 204  
 Db 507 TCBAATACATCCCTCCGCGCTGCTCTATGAGCTGCTTTGTCTTGGCTTATCTCA 448  
 Qy 205 ATGCACTAGTATATTCATCTTATACATTTTCAAAATGAGACCTTGAAGAGACCATCA 264  
 Db 447 ACGCCACAGCCCTGT---GGCTCTTCCTGAAGATGGGCGCTGGAACCCCAACCGTCT 391  
 Qy 265 TTATGCTGAACCTGGCTGCAACAGATCTGTATCTGACACAGCTCCCTTCTGATTC 324  
 Db 390 TCTGTGTCAACCTGGCTGCTCTCCGACTTCTCTACATTTCTGTGCTGCGCCACCTCATCT 331  
 Qy 325 ACTACTATGCGAGTGGCGGAAAAGTGAATCTTTGGAATTTGATGTGAATTTATCCGCT 384  
 Db 330 ACTATTAAGCCCAACACAGGCGACTGG-CTTGGCGGTGGACGCTGCAAAATGTGGCT 272  
 Qy 385 TCAGCTTCATTTCAACCTGTATAGAGACATCTCTTCTCCACCTGTTTACAGATCTTCC 444  
 Db 271 TCTCTTTTACGTTCAACCTCTTATGACAGATCTCTTCTCCTCATCTGATGAGGTATCC 212  
 Qy 445 GCTACTGTGTGATTCATTCACCCATGAGCTGCTTTTCCATTCACAAAATCGATGTCAG 504  
 Db 211 GTTACCTGGGCACTCTCCACCCGATTAAGCGCTGATCTGTGAANCCCGANATTCCT 152  
 Qy 505 TTGTAGCTGTGTGTGTGTGTGTATGATTCATTCATGCTGTGATCTTCATTCATGACCTTCT 564  
 Db 151 ACTGT 92  
 Qy 565 TGATCATCATCAACCAAGAGACAGATGAGCTGTCTGACCTCAACAGTTCGGA 622  
 Db 91 TTGTACACCTTCCAGCGGAGACATATCTCTGTGCAATGATACCAACGCCGGA 34

RESULT 8  
 BG712193 491 bp mRNA linear EST 08-MAY-2001  
 LOCUS pglin.pk011.f3 Normalized Liver Library Gallus gallus cdna clone  
 DEFINITION pglin.pk011.f3 5' similar to gp|A060339.1 (AF031897) G protein coupled P2Y nucleotide receptor [Melasgrus galllopavo]g, mRNA sequence.

ACCESSION BG712193 GI:14006135  
 VERSION BG712193.1  
 KEYWORDS EST.  
 SOURCE chicken.  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae; Gallus.

REFERENCE 1 (bases 1 to 491)  
 AUTHORS Burnside,J., Morgan,R.W. and Cogburn,L.A.  
 TITLE Chicken ESTs from a normalized liver library  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Joan Burnside  
 Molecular Endocrinology  
 University of Delaware  
 40 Townsend Hall, Newark, DE 19717, USA  
 Tel: 302 831-1345  
 Fax: 302-831-3411  
 Email: joan@udel.edu, www.chickest.udel.edu.

## FEATURES

source  
 1..491  
 /organism="Gallus gallus"  
 /db\_xref="taxon:9031"  
 /clone="pglin.pk011.f3"  
 /clone\_lib="Normalized Liver Library"  
 /sex="Male and Female"  
 /tissue type="liver"  
 /lab\_host="E.coli EMDH10B"

BASE COUNT 305 a 216 c 280 g 284 t 16 others  
 ORIGIN





Db 488 GATTCGTGAACCCCATGGGCAACCCAGAGAGAGCAACATCGCCGTTGGCTTCCTT 547  
 Qy 515 TGCTGNGGTGATCATTTCACTGATGAGTCGC 548  
 Db 548 GGCATCTGCTCTCTGATTTTCTGATCACCATC 581

## RESULT 15

A2953874

606 bp DNA 1linear GSS 27-APR-2001

A2953874

2M0219117F Mouse 10kb plasmid UUGC2M library Mus musculus genomic

A2953874

clone UUGC2M0219117 F, DNA sequence.

A2953874

GSS.

A2953874

GI:13825101

A2953874

house mouse.

A2953874

Mus musculus

A2953874

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

A2953874

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

A2953874

1 (bases 1 to 606)

A2953874

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

A2953874

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,

A2953874

M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.

A2953874

and Wright, D., Weiss, R.

A2953874

Mouse whole genome scaffolding with paired end reads from 10kb

A2953874

Plasmid inserts

A2953874

Unpublished (2000)

A2953874

Contact: Robert B. Weiss

A2953874

University of Utah Genome Center

A2953874

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

A2953874

84112, USA

A2953874

Tel: 801 585 5606

A2953874

Fax: 801 585 7177

A2953874

Email: ddunne@genetics.utah.edu

A2953874

Insert Length: 10000 Std Error: 0.00

A2953874

Plate: 0219 row: 1 column: 17

A2953874

Seq primer: GGTGTATAACGACGCGCAGT

A2953874

Class: plasmid ends

A2953874

High quality sequence stop: 606.

A2953874

Location/Qualifiers

A2953874

1. 606

A2953874

/organism="Mus musculus"

A2953874

/strain="C57BL/6J"

A2953874

/db\_xref="taxon:10090"

A2953874

/clone="UUGC2M0219117"

A2953874

/clone\_lib="Mouse 10kb plasmid UUGC2M library"

A2953874

/sex="Female"

A2953874

/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"

A2953874

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1473114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## BASE COUNT

100 a 203 c 145 g 158 t

## ORIGIN

Query Match

9.1%; Score 98.4; DB 17; Length 606;

Best Local Similarity 57.2%; Pred. No. 4e-17;  
 Matches 199; Conservative 0; Mismatches 146; Indels 3; Gaps 1;  
 Qy 270 CTGAACCTGGCTGCAAGATCTGCTGATCTGACAGCCTCCCTTCTGATTAACCTAC 329  
 Db 160 CTGAACCTGGCACTGGCGGACCTGATGATGCTGTTCACTACCCCTACTATCTATAC 219  
 Qy 330 TATGCAATGGGCAAACTGATCTTGGAGATTTATGATGATTTATCCGCTTACG 389  
 Db 220 TACGCCAGATGGACCACTGGCCCTTGGAGACCTGGCCGCTTGGACCTTCTTC 279  
 Qy 390 TTCCATTTCACTGATGATGACAGCATCTTCTGACCTGTTTCAAGATCTTCCGCTAC 449  
 Db 280 TTCTATGCCATCTATATGACAGCATCTTCTTCTCACTGATGATGATGATGATGAT 339  
 Qy 450 TGTGATCATTCACCCAAATGAGCTGCTTTCATTCACAAAATGATGATGATGATGAT 506  
 Db 340 CTGGGATCTGGCAACCCCTGGCTTCTTGGCAACAGCTGGAAGTGGCCGTGCTTGG 399  
 Qy 507 GTAGCTGCTGCTGCTGCTGATCATTTCACTGATGATGATGATGATGATGATGATGAT 566  
 Db 400 GTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 459  
 Qy 567 ATCAATCAACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 614  
 Db 460 GCTGCCAATGATCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 507

Search completed: January 30, 2003, 11:05:45  
 Job time : 2204 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 03:10:53 ; Search time 59 Seconds  
(without alignments)

5618.942 Million cell updates/sec

Title: US-10-010-568-1

Sequence: 1 catatgcacaaactgaactc.....ccttgaataattcattac 1081

Scoring table: IDENTITY NUC  
Gapop 10-0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:  
1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match length	ID	Description
1	129	11.9	1996	2	US-08-559-524A-1 Sequence 1, Appl
2	129	11.9	1996	3	US-08-749-707-1 Sequence 1, Appl
3	103.2	9.5	1842	1	US-08-442-134A-1 Sequence 1, Appl
4	103.2	9.5	1842	1	US-08-444-581B-1 Sequence 1, Appl
5	103.2	9.5	1842	1	US-08-446-088A-1 Sequence 1, Appl
6	100	9.3	984	3	US-08-513-974B-41 Sequence 41, Appl
7	100	9.3	1020	3	US-08-513-974B-370 Sequence 370, App
8	97.8	9.0	1475	1	US-08-097-938-1 Sequence 1, Appl
9	97.8	9.0	1475	1	US-08-476-000-1 Sequence 1, Appl
10	97.8	9.0	1475	1	US-08-472-840-1 Sequence 1, Appl
11	97.8	9.0	1475	2	US-08-476-976-1 Sequence 1, Appl
12	97.8	9.0	1475	2	US-08-474-410-1 Sequence 1, Appl
13	97.8	9.0	1475	4	US-08-486-673B-1 Sequence 1, Appl
14	97.8	9.0	2732	1	US-08-476-000-60 Sequence 60, Appl
15	97.8	9.0	2732	1	US-08-472-840-60 Sequence 60, Appl
16	97.8	9.0	2732	2	US-08-476-976-60 Sequence 60, Appl
17	97.8	9.0	2732	3	US-08-474-410-60 Sequence 60, Appl
18	97.8	9.0	2732	4	US-08-486-673B-60 Sequence 60, Appl
19	95.8	8.9	984	3	US-08-513-974B-57 Sequence 57, Appl
20	95.8	8.9	1023	3	US-08-513-974B-379 Sequence 379, App
21	94.2	8.7	984	3	US-08-459-046-1 Sequence 1, Appl
22	92.8	8.6	1102	2	US-08-742-440A-5 Sequence 5, Appl
23	92.8	8.6	1224	2	US-08-742-440A-4 Sequence 4, Appl
24	90.8	8.4	1901	1	US-08-153-848-43 Sequence 43, Appl
25	90.8	8.4	1901	3	US-09-239-843A-43 Sequence 43, Appl
26	90.8	8.4	1901	4	US-09-088-337B-43 Sequence 43, Appl
27	90.8	8.4	1901	5	PCT-US93-11153-43 Sequence 43, Appl

28	90.8	8.4	2453	5	PCT-US95-07180-1 Sequence 1, Appl
29	87.2	8.1	1224	2	US-08-742-440A-1 Sequence 1, Appl
30	84	7.8	1317	1	US-08-153-848-45 Sequence 45, Appl
31	84	7.8	1317	3	US-09-299-843A-45 Sequence 45, Appl
32	84	7.8	1317	5	US-09-088-337B-45 Sequence 45, Appl
33	84	7.8	1317	5	PCT-US93-11153-45 Sequence 45, Appl
34	84	7.8	1664	4	US-09-582-224A-5 Sequence 5, Appl
35	84	7.8	1679	4	US-09-517-605-14 Sequence 14, Appl
36	84	7.8	1737	1	US-08-202-056-4 Sequence 4, Appl
37	84	7.8	1737	1	US-08-076-093A-3 Sequence 3, Appl
38	84	7.8	1737	2	US-08-701-265-3 Sequence 3, Appl
39	84	7.8	1737	2	US-08-284-586-3 Sequence 3, Appl
40	84	7.8	1737	2	US-08-805-478-3 Sequence 3, Appl
41	84	7.8	1737	2	US-08-802-627A-3 Sequence 3, Appl
42	84	7.8	1737	2	US-08-801-238-3 Sequence 3, Appl
43	84	7.8	1737	2	US-08-801-228-3 Sequence 3, Appl
44	84	7.8	1737	3	US-09-104-296-3 Sequence 3, Appl
45	84	7.8	1737	5	PCT-US94-06380-2 Sequence 2, Appl

#### ALIGNMENTS

RESULT 1  
US-08-559-524A-1  
Sequence 1, Application US/08559524A  
Patent No. 5871963  
GENERAL INFORMATION:  
APPLICANT: Conley, Pamela B.  
APPLICANT: Jantzen, Hans-Michael  
TITLE OF INVENTION: NOVEL PORINERGIC RECEPTOR  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP  
STREET: 1800 M Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20036-5869  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/559,524A  
FILING DATE: 15-NOV-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Adler, Reid G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: 044481-5010-00-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-467-7000  
TELEFAX: 202-467-7176  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1996 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 625..1626  
US-08-559-524A-1  
Query Match 11.9%; Score 129; DB 2; Length 1996;  
Best Local Similarity 50.1%; Pred. No. 1,48-29;  
Matches 380; Conservative 0; Mismatches 370; Indels 9; Gaps 2;  
QY 108 GCGCTTTGGAAATGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTT 167





APPLICATION NUMBER: PCT/JP95/01599  
FILING DATE: 10-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-093989  
FILING DATE: 19-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-057186  
FILING DATE: 16-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-007177  
FILING DATE: 20-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-326611  
FILING DATE: 28-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-270017  
FILING DATE: 02-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236357  
FILING DATE: 30-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236356  
FILING DATE: 30-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189274  
FILING DATE: 11-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189273  
FILING DATE: 11-AUG-1945  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189272  
FILING DATE: 11-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Resnick, David S.  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 45753  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 984 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-513-974B-41

Query Match 9.3%; Score 100; DB 3; Length 984;  
Best Local Similarity 57.5%; Pred. No. 7.2e-21;  
Matches 200; Conservative 0; Mismatches 145; Indels 3; Gaps 1;  
QY 270 CTGAACCTGGCGCTGACAGATGCTGATCTGACACGCTCCCTTCTGATTTACATAC 329  
DB 196 CTGAACCTGGCGCTGACAGATGCTGATCTGACACGCTCCCTTCTGATTTACATAC 255  
QY 330 TATCCAGTGGCGAAAATGGATCTTTGAGATTTTCATGTAAGTTATTCGGCTTACG 389  
DB 256 TAGCCAGAGGGAACCACTGCGCTTGGAGACCTGCGCTTGTGAGCTTCTC 315  
QY 390 TTCCATTTCAACCTGTATAGAGAGATCTCTTCTCACTGCTTTTCAGATCTTCCGCTAC 449  
DB 316 TTCTATGCCAATTAACATGAGACATCTGTTCCCACTGATTAAGTTCCAGGCTAC 375  
QY 450 TGTGTATCATTCACCCATAGAGCTGCTTTTCATTCACAAACTCGATGTCAGTT--- 506  
DB 376 CTGGGCACTGCGACCCCTGCTCTCCGCAAGCTGAGGTCGCGGCTGCTGG 435  
QY 507 GTAGCCGTGCTGTGATGATGATTTCACTGTGAGTGTTCATTCGATACCTTCTTG 566  
DB 436 GTAGTGTGTGAGATGCTGTGCTGCTGTGACAGCCAGTGTCTGCGCAGGAGTCTTT 495  
QY 567 ATGACATCAACCAACAGAGCAAGATCAAGATCAAGCTGTCTGACCTGACC 614

DB 496 GCTGCCAGGCAATCCAGCGCAACCGCACTGTGTCTACGACCTGAGC 543  
RESULT 7  
US-08-513-974B-370  
Sequence 370, Application US/08513974B  
Patent No. 6114139  
GENERAL INFORMATION:  
APPLICANT: Hinuma, Shuji  
APPLICANT: Hosoya, Masaki  
APPLICANT: Fujii, Ryo  
APPLICANT: Ohtaki, Tetsuya  
APPLICANT: Fukusumi, Shoji  
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
NUMBER OF SEQUENCES: 380  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIXE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/513,974B  
FILING DATE: 14-SEP-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP95/01599  
FILING DATE: 10-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-093989  
FILING DATE: 19-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-057186  
FILING DATE: 16-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-007177  
FILING DATE: 20-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-326611  
FILING DATE: 28-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-270017  
FILING DATE: 02-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236357  
FILING DATE: 30-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236356  
FILING DATE: 30-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189274  
FILING DATE: 11-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189273  
FILING DATE: 11-AUG-1945  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189272  
FILING DATE: 11-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Resnick, David S.  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 45753  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400

FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/390,301  
FILING DATE: 25-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: ADLER, REID G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: 2803-0006.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1475 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 232..1416  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 232  
US-08-476-000-1

Query Match 9.0%; Score 97.8; DB 1; Length 1475;  
Best Local Similarity 52.6%; Pred. No. 4.3e-20;  
Matches 213; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

QY 144 CTCAGATGACCTACCTCCCTGTTATTATGAGATATCTCTCCGCGGATTTCCAGGC 203  
DB 442 CTGACACGAGCTTTCTTCGGTCGTCTACATTATGTTGATGTTGGCCAGT 501  
QY 204 AATGCAATGATATTCACCTTACATTTTCAAAATGAGACCTTGAAGAGACAGACATC 263  
DB 502 AATGCAATGAGCCCTCGATCTTCTTCCGACGAAAGAAACACCCCGCGGATT 561  
QY 264 ATTATGCTGAACCTGGCTGCAAGATCTGCTGATCTGACGACCTCCCTTCTGATT 323  
DB 562 TACATGGCCAACTGGCCCTGGCCGACCTCTCTGTCATCTGTTCCCTCGAAGATC 621  
QY 324 CACTACTATGCAAGTGGGCAAAATGAGATCTTGAAGATTTCACTGTGTAAGTTATCCGC 383  
DB 622 TCTTACACCTTACATGGAACAACCTGGGTCTAGCGGAGAGCCCTCTGCAAGGTCTCAT 681  
QY 384 TTCAAGCTTCATTCAACCTGATATGACAGATCTCTCTCACTGTTTACGATCTTC 443  
DB 682 GGCCTTTTCTATGTAACATGATATGCTCCATCTCTTATGACCTGCTCAAGCGTGACG 741  
QY 444 CGTACTGTGTGATCATTCACCCAAATGAGCTGCTTTTCCATTCAAAATCGATGTGA 503  
DB 742 AGTACTGGGTGATGTGAACCCCATGGAGACCCAGAGAAAGGCAAAACATGCGCGT 801  
QY 504 GTTGTAGCTGTGCTGTGTGTGATCATTTTCACTGTGATGCTGTG 548  
DB 802 GCGCTCTCTTGGCAATCTGGCTCTGATTTTCTGTGATCAACATC 846

RESULT 10  
US-08-472-840-1  
Sequence 1, Application US/08472840  
Patent No. 5763575  
GENERAL INFORMATION:  
APPLICANT: SUNDELIN, JOHAN  
APPLICANT: SCARBOROUGH, ROBERT M.  
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS  
TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500

CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE:  
APPLICATION NUMBER: US/08/472,840  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,301  
FILING DATE: 25-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: ADLER, REID G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: 2803-0006.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1475 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 232..1416  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 232  
US-08-472-840-1

Query Match 9.0%; Score 97.8; DB 1; Length 1475;  
Best Local Similarity 52.6%; Pred. No. 4.3e-20;  
Matches 213; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

QY 144 CTCAGATGACCTACCTCCCTGTTATTATGAGATATCTCTCCGCGGATTTCCAGGC 203  
DB 442 CTGACACGAGCTTTCTTCGGTCGTCTACATTATGTTGATGTTGGCCAGT 501  
QY 204 AATGCAATGATATTCACCTTACATTTTCAAAATGAGACCTTGAAGAGACAGACATC 263  
DB 502 AATGCAATGAGCCCTCGATCTTCTTCCGACGAAAGAAACACCCCGCGGATT 561  
QY 264 ATTATGCTGAACCTGGCTGCAAGATCTGCTGATCTGACGACCTCCCTTCTGATT 323  
DB 562 TACATGGCCAACTGGCCCTGGCCGACCTCTCTGTCATCTGTTCCCTCGAAGATC 621  
QY 324 CACTACTATGCAAGTGGGCAAAATGAGATCTTGAAGATTTCACTGTGTAAGTTATCCGC 383  
DB 622 TCTTACACCTTACATGGAACAACCTGGGTCTAGCGGAGAGCCCTCTGCAAGGTCTCAT 681  
QY 384 TTCAAGCTTCATTCAACCTGATATGACAGATCTCTCTCACTGTTTACGATCTTC 443  
DB 682 GGCCTTTTCTATGTAACATGATATGCTCCATCTCTTATGACCTGCTCAAGCGTGACG 741  
QY 444 CGTACTGTGTGATCATTCACCCAAATGAGCTGCTTTTCCATTCAAAATCGATGTGA 503  
DB 742 AGTACTGGGTGATGTGAACCCCATGGAGACCCAGAGAAAGGCAAAACATGCGCGT 801  
QY 504 GTTGTAGCTGTGCTGTGTGTGATCATTTTCACTGTGATGCTGTG 548  
DB 802 GCGCTCTCTTGGCAATCTGGCTCTGATTTTCTGTGATCAACATC 846

RESULT 11  
US-08-476-976-1



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 04:05:55 Search time 69 Seconds  
(without alignments)  
7038.482 Million cell updates/sec

Title: US-10-010-568-1  
Perfect score: 1081

Sequence: 1 catatgcgaactgaactc.....ccttgaataattcattac 1081

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 396772 seqs, 224632407 residues

Total number of hits satisfying chosen parameters: 793544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

#### Database :

Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/ECT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/ECTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1014	93.8	1014	US-09-943-798-3	Sequence 3, Appl1
2	831	76.9	831	US-09-943-798-1	Sequence 1, Appl1
3	779.4	72.1	1313	US-09-728-422-1	Sequence 1, Appl1
4	515	47.6	526	US-09-812-102-40	Sequence 40, Appl1
5	93.6	8.7	993	US-09-826-791-1	Sequence 1, Appl1
6	93.6	8.7	1041	US-09-826-791-5	Sequence 5, Appl1
7	93.6	8.7	1041	US-09-826-791-5	Sequence 5, Appl1
8	93.6	8.7	1041	US-09-826-791-5	Sequence 5, Appl1
9	93.6	8.7	1041	US-09-826-791-5	Sequence 5, Appl1
10	93.6	8.7	1041	US-09-826-791-5	Sequence 5, Appl1
11	90.8	8.4	1020	US-09-728-952-26	Sequence 26, Appl1
12	84	7.8	1670	US-09-880-107-4143	Sequence 2143, Appl1
13	84	7.8	1670	US-09-880-107-4143	Sequence 2143, Appl1
14	82.8	7.7	2051	US-09-962-832-218	Sequence 218, Appl1
15	82.8	7.7	2051	US-09-962-832-218	Sequence 218, Appl1
16	82.6	7.6	1065	US-09-922-895-2	Sequence 2, Appl1
17	82.6	7.6	1689	US-09-921-381A-15	Sequence 15, Appl1
18	82.6	7.6	1717	US-09-964-824A-100	Sequence 100, Appl1
19	82.6	7.6	1915	US-10-106-623-3	Sequence 3, Appl1

20	82.6	7.6	3426	US-10-001-835-29	Sequence 29, Appl1
21	82.4	7.6	1080	US-09-739-151-1	Sequence 1, Appl1
22	82.4	7.6	1102	US-09-870-759-143	Sequence 143, Appl1
23	82.4	7.6	1955	US-10-190-469-2	Sequence 2, Appl1
24	81.6	7.5	2050	US-09-940-240-15	Sequence 15, Appl1
25	77.2	7.1	1083	US-09-852-156-7	Sequence 7, Appl1
26	74	6.8	1895	US-09-940-240-19	Sequence 19, Appl1
27	73.8	6.8	1083	US-09-852-156-11	Sequence 11, Appl1
28	73.4	6.8	1910	US-09-944-807-1	Sequence 1, Appl1
29	73.4	6.8	2080	US-10-044-090-628	Sequence 628, Appl1
30	73.2	6.8	2081	US-10-044-090-627	Sequence 627, Appl1
31	73.2	6.8	1860	US-09-940-240-17	Sequence 17, Appl1
32	72.4	6.7	823	US-10-044-090-598	Sequence 598, Appl1
33	72.4	6.7	993	US-09-826-508-15	Sequence 15, Appl1
34	72.4	6.7	993	US-09-954-456-1129	Sequence 1129, Appl1
35	72.4	6.7	1414	US-10-098-841-312	Sequence 312, Appl1
36	71.8	6.6	1892	US-09-908-699A-1	Sequence 1, Appl1
37	71.4	6.6	1563	US-09-880-107-1611	Sequence 1611, Appl1
38	70.6	6.5	1083	US-09-852-156-9	Sequence 9, Appl1
39	69.8	6.5	1080	US-09-867-915-2	Sequence 2, Appl1
40	69.8	6.5	2268	US-09-867-915-1	Sequence 3034, Appl1
41	69.8	6.5	2632	US-09-867-915-1	Sequence 1, Appl1
42	69.8	6.5	2632	US-09-867-915-26	Sequence 26, Appl1
43	69.6	6.4	1014	US-09-791-932-55	Sequence 55, Appl1
44	69.6	6.4	1464	US-10-166-359-1	Sequence 1, Appl1
45	69.6	6.4	1464	US-10-166-359-1	Sequence 1, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-943-798-3  
Sequence 3, Application US/09943798  
Patent No. US20020065215A1  
GENERAL INFORMATION:  
APPLICANT: Glaxo Group Limited  
TITLE OF INVENTION: Polypeptide  
FILE REFERENCE: QG1021  
CURRENT APPLICATION NUMBER: US/09/943,798  
CURRENT FILING DATE: 2001-08-31  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 1014  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-943-798-3

Query Match 93.8%; Score 1014; DB 10; Length 1014;  
Best Local Similarity 100.0%; Pred. No. 9.2e-291;  
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	54	ATGATGAGCAGCTAGACTATTATTAGCAATGCTTCTGATTTCCCGATTATGAGCTGCT	113
DB	1	ATGATGAGCAGCTAGACTATTATTAGCAATGCTTCTGATTTCCCGATTATGAGCTGCT	60
QY	114	TTTGAAATTTGACCTGATGAAAAATCCCACTCAATGACCTACCTCTGTTATTAT	173
DB	61	TTTGAAATTTGACCTGATGAAAAATCCCACTCAATGACCTACCTCTGTTATTAT	120
QY	174	GSCATATCTTCCTGCTGGATTTTCCAGGCAATGAGTGTGATTCACCTTACATTTTC	233
DB	121	GSCATATCTTCCTGCTGGATTTTCCAGGCAATGAGTGTGATTCACCTTACATTTTC	180
QY	234	AAATGAGCCTTGAAGAGCAGCAGCATATTATGCTAACTGCTGCAAGATCTG	293
DB	181	AAATGAGCCTTGAAGAGCAGCAGCATATTATGCTAACTGCTGCAAGATCTG	240
QY	294	CTGTATCTGACAGCCTCCCTTCTGATTCATCTATGACGATGGGAAACTGGATC	353
DB	241	CTGTATCTGACAGCCTCCCTTCTGATTCATCTATGACGATGGGAAACTGGATC	300

```
; CURRENT APPLICATION NUMBER: US/09/728,422
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: pc_fl_genes Version 2.0
; SEQ ID NO 1
; LENGTH: 1313
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (547)..(1239)
US-09-728-422-1

Query Match          72.1%; Score 779.4; DB 10; Length 1313;
Best Local Similarity 99.6%; Pred. No. 4e-221;
Matches 792; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 CATATTGCCAACTGAACCTCTCTTTCTTGTGCAAGTGAAGAGACAAACATGAATG 60
DB 494 CATATTGCCAACTGAACCTCTCTTTCTTGTGCAAGTGAAGAGACAAACATGAATG 553
QY 61 AGCCACTAGACTATTAGCAAAATGCTCTGATTTCCCGAATTAGCAGCTGTTTGGAA 120
DB 554 AGCCACTAGACTATTAGCAAAATGCTCTGATTTCCCGAATTAGCAGCTGTTTGGAA 613
QY 121 ATTGCACTGATGAAAATCATCCCACTCAAGATGACACTACCTCCCTGTTATTATGACATTA 180
DB 614 ATTGCACTGATGAAAATCATCCCACTCAAGATGACACTACCTCCCTGTTATTATGACATTA 673
QY 181 TCTTCTCTGGGATTTCCAGGCAAGCAGATGATATTCATTAATTTCAAAATGA 240
DB 674 TCTTCTCTGGGATTTCCAGGCAAGCAGATGATATTCATTAATTTCAAAATGA 733
QY 241 GACCTTGAAGAGACACATCATATTATGCTGAACCTGGCTGACAGATCTGCTATATC 300
DB 734 GACCTTGAAGAGACACATCATATTATGCTGAACCTGGCTGACAGATCTGCTATATC 793
QY 301 TGAACAGCTCCCTCTCTGATTCATCTACTATGCGAGTGGGAAAATGAGATCTTTGGAG 360
DB 794 TGAACAGCTCCCTCTCTGATTCATCTACTATGCGAGTGGGAAAATGAGATCTTTGGAG 853
QY 361 ATTTCATGTAAGTTATTCGCTTCAAGCTTCAATTTCAACCTGTATAGACATCTCTCT 420
DB 854 ATTTCATGTAAGTTATTCGCTTCAAGCTTCAATTTCAACCTGTATAGACATCTCTCT 913
QY 421 TCTTCACTGTTTACGATCTTCGCTACTGCTGATCATTTCAACCAATGAGCTGCTTTT 480
DB 914 TCTTCACTGTTTACGATCTTCGCTACTGCTGATCATTTCAACCAATGAGCTGCTTTT 973
QY 481 CCATTTCACAAATCGATGAGTGTAGACCTGTGCTGTGTGTGATCATTTCACTGG 540
DB 974 CCATTTCACAAATCGATGAGTGTAGACCTGTGCTGTGTGTGATCATTTCACTGG 1033
QY 541 TAGCTGTCAATTCGATGACCTTTCTGTATCATCAACCAAGAGACCAAGATCGACCT 600
DB 1034 TAGCTGTCAATTCGATGACCTTTCTGTATCATCAACCAAGAGACCAAGATCGACCT 1093
QY 601 GTCTGACCTCAACAGTGGATGAATCAATATTAATTAAGTGTGTAACCTGATTTTGA 660
DB 1094 GTCTGACCTCAACAGTGGATGAATCAATATTAATTAAGTGTGTAACCTGATTTTGA 1153
QY 661 CTGCAACTACTTTTCTGCTCCCTCTGGTGTAGTGTAGACATTTGCTATACAGATTAATCC 720
DB 1154 CTGCAACTACTTTTCTGCTCCCTCTGGTGTAGTGTAGACATTTGCTATACAGATTAATCC 1211
QY 721 AACTCTGACCACTGACCTGCAAACTGACAGCTGCTTAAAGCAAGAAAGCAGAGGCTAA 780
DB 1212 AACTCTGACCACTGACCTGCAAACTGACAGCTGCTTAAAGCAAGAAAGCAGAGGCTAA 1271
```

```
QY 781 CCATTCTGCTACTCC 795
DB 1272 CCATTCTGCTACTCC 1286

RESULT 4
US-09-812-102-40/c
; Sequence 40; Application US/09812102
; Patent No. US2002005179A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Kelch B
; TITLE OF INVENTION: No. US2002005179A1e1 G-Protein Coupled Receptor Homologs
; FILE REFERENCE: 5800-41 035800/183478
; CURRENT APPLICATION NUMBER: US/09/812,102
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/09/364,769
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: GPCR-RHODOPSIN
US-09-812-102-40

Query Match          47.6%; Score 515; DB 10; Length 526;
Best Local Similarity 100.0%; Pred. No. 6.3e-143;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 CCCTCTCTGATTCATCTATGCGAGTGGCGAAAATGATGATCTTTGAGATTCATGTGT 371
DB 526 CCCTCTCTGATTCATCTATGCGAGTGGCGAAAATGATGATCTTTGAGATTCATGTGT 467
QY 372 AAGTTATTCGCTTCACTGCTTCAATTTCAACCTGTATAGACATCTCTTCTCACTGT 431
DB 466 AAGTTATTCGCTTCACTGCTTCAATTTCAACCTGTATAGACATCTCTTCTCACTGT 407
QY 432 TTGAGCATCTTCGCTACTAGTGTGATCATTTCAACCAATGAGCTGTTTGCATTCAGAAA 491
DB 406 TTGAGCATCTTCGCTACTAGTGTGATCATTTCAACCAATGAGCTGTTTGCATTCAGAAA 347
QY 492 ACTGATGTCAGTGTGAGCTGTGCTGTGTGTGTGATCATTTCACTGTGATGTGATTT 551
DB 346 ACTGATGTCAGTGTGAGCTGTGCTGTGTGTGTGATCATTTCACTGTGATGTGATTT 287
QY 552 CCGATGACCTTTGATCATCAACCAAGAGACCAAGATGAGCTGTGTGACCTTC 611
DB 286 CCGATGACCTTTGATCATCAACCAAGAGACCAAGATGAGCTGTGTGACCTTC 227
QY 612 ACCAGTTCGATGATCACTATTAATAGTGTGTAACCACTGATTTTGAAGTCACTACT 671
DB 226 ACCAGTTCGATGATCACTATTAATAGTGTGTAACCACTGATTTTGAAGTCACTACT 167
QY 672 TTCTGCTCCCTCTGGATGATGACATTTGCTATACAGATTAATACCACTGACCTGACC 731
DB 166 TTCTGCTCCCTCTGGATGATGACATTTGCTATACAGATTAATACCACTGACCTGACC 107
QY 732 CATGACCTGCAAACTGACAGCTGCTTTAAGCAGAAAGCAGAAAGCTTAACATTTCTGTA 791
DB 106 CATGACCTGCAAACTGACAGCTGCTTTAAGCAGAAAGCAGAAAGCTTAACATTTCTGTA 47
QY 792 CTCCTTGATTTTATAGTATGTTTATTAACCTTCCA 826
DB 46 CTCCTTGATTTTATAGTATGTTTATTAACCTTCCA 12

RESULT 5
US-09-826-791-1
; Sequence 1; Application US/09826791
; Patent No. US20010039037A1
; GENERAL INFORMATION:
```









SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 1  
 LENGTH: 1081  
 TYPE: DNA  
 ORGANISM: homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (54)..(1067)  
 US-60-251-926-1

Query Match 100.0%; Score 1081; DB 69; Length 1081;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-299;  
 Matches 1081; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTTGCAAACTGAACTCTCTGTTTCTTGGCAAGTGAAGGAGCAACCATGATG 60  
 DB 1 CATTTGCAAACTGAACTCTCTGTTTCTTGGCAAGTGAAGGAGCAACCATGATG 60  
 QY 61 AGCCACTAGACTATTATGCAAAATGCTTCTGATTTCCCGAATTATGACCTGCTTTGGAA 120  
 DB 61 AGCCACTAGACTATTATGCAAAATGCTTCTGATTTCCCGAATTATGACCTGCTTTGGAA 120  
 QY 121 ATTGCACTGATGAAAACATCCCACTCAAGATGACACTACCTCCCTGTTATTTATGCAATTA 180  
 DB 121 ATTGCACTGATGAAAACATCCCACTCAAGATGACACTACCTCCCTGTTATTTATGCAATTA 180  
 QY 181 TCTTCCGCGGGGATTTCCAGGCAATGCAATGATATCCACTTACATTTTCAAAATGA 240  
 DB 181 TCTTCCGCGGGGATTTCCAGGCAATGCAATGATATCCACTTACATTTTCAAAATGA 240  
 QY 241 GACCTTGAAGAGAGAGACCATCATTTATGCTGAACCTGCGCTGCAAGATCGCTGTATC 300  
 DB 241 GACCTTGAAGAGAGAGACCATCATTTATGCTGAACCTGCGCTGCAAGATCGCTGTATC 300  
 QY 301 TGAACAGCCTCCCTTCTCTGATTCATATATGCGAGTGGCGAAAATGATCTTTGGAG 360  
 DB 301 TGAACAGCCTCCCTTCTCTGATTCATATATGCGAGTGGCGAAAATGATCTTTGGAG 360  
 QY 361 ATTTCATGATGATTTATTCGGCTTCAGCTTCACCTTTCAACCTGTATGACGATCTCT 420  
 DB 361 ATTTCATGATGATTTATTCGGCTTCAGCTTCACCTTTCAACCTGTATGACGATCTCT 420  
 QY 421 TCTTCACTGTTTCAAGCATCTTCGGCTACTGATGATCATCCCAATGAGCGCTTTT 480  
 DB 421 TCTTCACTGTTTCAAGCATCTTCGGCTACTGATGATCATCCCAATGAGCGCTTTT 480  
 QY 481 CCATTCAAAAATCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540  
 DB 481 CCATTCAAAAATCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540  
 QY 541 TAGCTGTATTCGGATGACCTTCTTGTATCATCAACCAAGGACCAAGATCAGCT 600  
 DB 541 TAGCTGTATTCGGATGACCTTCTTGTATCATCAACCAAGGACCAAGATCAGCT 600  
 QY 601 GTCTGACCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660  
 DB 601 GTCTGACCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660  
 QY 661 CTGCAACTATCTTCTGCTCCCTTGGATGATGATGATGATGATGATGATGATGATGATG 720  
 DB 661 CTGCAACTATCTTCTGCTCCCTTGGATGATGATGATGATGATGATGATGATGATGATG 720  
 QY 721 ACACTGTGACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780  
 DB 721 ACACTGTGACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780  
 QY 781 CCATTCTGCTACTCTTCTGATTTTATGATGATGATGATGATGATGATGATGATGATG 840  
 DB 781 CCATTCTGCTACTCTTCTGATTTTATGATGATGATGATGATGATGATGATGATGATG 840  
 QY 841 TTGGATGCAATCTGCGCTGCTTCAATGATGATGATGATGATGATGATGATGATGATG 900  
 DB 841 TTGGATGCAATCTGCGCTGCTTCAATGATGATGATGATGATGATGATGATGATGATG 900

QY 901 CTATACGTTTCTAGACCATTAAGCTGCTGAAACACTTTGATACCTGTTACTATATG 960  
 DB 901 CTATACGTTTCTAGACCATTAAGCTGCTGAAACACTTTGATACCTGTTACTATATG 960  
 QY 961 TGTGTGAGGAGCAAACTTTAGAGAGGCTGCTGCTCAACAGTATGATGAAAGTAAAGG 1020  
 DB 961 TGTGTGAGGAGCAAACTTTAGAGAGGCTGCTGCTCAACAGTATGATGAAAGTAAAGG 1020  
 QY 1021 GAACTTTGAGCAAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1080  
 DB 1021 GAACTTTGAGCAAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1080  
 QY 1081 C 1081  
 DB 1081 C 1081

RESULT 3  
 US-60-269-795-1  
 Sequence 1, Application US/60269795  
 GENERAL INFORMATION:  
 APPLICANT: Bristol-Myers Squibb Company  
 TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGRPM23, EXPRE  
 TITLE OF INVENTION: KIDNEY  
 FILE REFERENCE: D0077 PSP 1  
 CURRENT APPLICATION NUMBER: US/60/269,795  
 CURRENT FILING DATE: 2001-02-14  
 NUMBER OF SEQ ID NOS: 35  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 1  
 LENGTH: 1081  
 TYPE: DNA  
 ORGANISM: homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (54)..(1064)  
 US-60-269-795-1

Query Match 100.0%; Score 1081; DB 70; Length 1081;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-299;  
 Matches 1081; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTTGCAAACTGAACTCTCTGTTTCTTGGCAAGTGAAGGAGCAACCATGATG 60  
 DB 1 CATTTGCAAACTGAACTCTCTGTTTCTTGGCAAGTGAAGGAGCAACCATGATG 60  
 QY 61 AGCCACTAGACTATTATGCAAAATGCTTCTGATTTCCCGAATTATGACCTGCTTTGGAA 120  
 DB 61 AGCCACTAGACTATTATGCAAAATGCTTCTGATTTCCCGAATTATGACCTGCTTTGGAA 120  
 QY 121 ATTGCACTGATGAAAACATCCCACTCAAGATGACACTACCTCCCTGTTATTTATGCAATTA 180  
 DB 121 ATTGCACTGATGAAAACATCCCACTCAAGATGACACTACCTCCCTGTTATTTATGCAATTA 180  
 QY 181 TCTTCCGCGGGGATTTCCAGGCAATGCAATGATATCCACTTACATTTTCAAAATGA 240  
 DB 181 TCTTCCGCGGGGATTTCCAGGCAATGCAATGATATCCACTTACATTTTCAAAATGA 240  
 QY 241 GACCTTGAAGAGAGAGACCATCATTTATGCTGAACCTGCGCTGCAAGATCGCTGTATC 300  
 DB 241 GACCTTGAAGAGAGAGACCATCATTTATGCTGAACCTGCGCTGCAAGATCGCTGTATC 300  
 QY 301 TGAACAGCCTCCCTTCTCTGATTCATATATGCGAGTGGCGAAAATGATCTTTGGAG 360  
 DB 301 TGAACAGCCTCCCTTCTCTGATTCATATATGCGAGTGGCGAAAATGATCTTTGGAG 360  
 QY 361 ATTTCATGATGATTTATTCGGCTTCAGCTTCACCTTTCAACCTGTATGACGATCTCT 420  
 DB 361 ATTTCATGATGATTTATTCGGCTTCAGCTTCACCTTTCAACCTGTATGACGATCTCT 420  
 QY 421 TCTTCACTGTTTCAAGCATCTTCGGCTACTGATGATCATCCCAATGAGCGCTTTT 480  
 DB 421 TCTTCACTGTTTCAAGCATCTTCGGCTACTGATGATCATCCCAATGAGCGCTTTT 480





Oy 961 TGGTGTGACGCAAACTTTAGAGAGGCTGTCTCTCAACAGTAGAGTAGCAAGTAAAGTAAAGCG 1020  
 Db 1201 TGGTGTGACGCAAACTTTAGAGAGGCTGTCTCTCAACAGTAGAGTAGCAAGTAAAGTAAAGCG 1260  
 Oy 1021 GGAACCTTGAGCAAGCAAGAAATTAAGTAACTCAAAACAACTTTGAATATTTCAATTA 1080  
 Db 1261 GGAACCTTGAGCAAGCAAGAAATTAAGTAACTCAAAACAACTTTGAATATTTCAATTA 1320  
 Oy 1081 C 1081  
 Db 1321 C 1321

RESULT 10  
 US-09-785-276A-30042  
 ; Sequence 30042, Application US/09785276A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schlegel, Robert  
 ; APPLICANT: Endege, Wilson  
 ; APPLICANT: Monahan, John  
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR  
 ; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF  
 ; FILE REFERENCE: HUMAN PROSTATE CANCER  
 ; FILE REFERENCE: MRI-007B  
 ; CURRENT APPLICATION NUMBER: US/09/785,276A  
 ; PRIOR FILING DATE: 2001-02-16  
 ; PRIOR APPLICATION NUMBER: 60/183,319  
 ; PRIOR FILING DATE: 2000-02-17  
 ; PRIOR APPLICATION NUMBER: 60/189,862  
 ; PRIOR FILING DATE: 2000-03-16  
 ; PRIOR APPLICATION NUMBER: 60/207,454  
 ; PRIOR FILING DATE: 2000-05-25  
 ; PRIOR APPLICATION NUMBER: 60/211,314  
 ; PRIOR FILING DATE: 2000-06-09  
 ; PRIOR APPLICATION NUMBER: 60/219,007  
 ; PRIOR FILING DATE: 2000-07-18  
 ; PRIOR APPLICATION NUMBER: 60/255,281  
 ; PRIOR FILING DATE: 2000-12-13  
 ; NUMBER OF SEQ ID NOS: 62232  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 30042  
 ; LENGTH: 1729  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc.feature  
 ; LOCATION: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-09-785-276A-30042

Query Match 99.9%; Score 1079.4; DB 30; Length 1729;  
 Best Local Similarity 99.9%; Pred. No. 6.2e-299;  
 Matches 1080; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 CATATTGCCAAATGAACTCTCTCTTTTCTTGAAGATGAAAGAGACAACATGATG 60  
 Db 241 CATATTGCCAAATGAACTCTCTCTTTTCTTGAAGATGAAAGAGACAACATGATG 300  
 Oy 61 AGCCACTAGACTATTAGCAAAATGCTTGTATTTCCCGCATTTATGACGCTGCTTTGAA 120  
 Db 301 AGCCACTAGACTATTAGCAAAATGCTTGTATTTCCCGCATTTATGACGCTGCTTTGAA 360  
 Oy 121 ATTGACTGATGAAAAATCCCACTCAAGATGACTACCTCCCTGTTATTTATGGAATTA 180  
 Db 361 ATTGACTGATGAAAAATCCCACTCAAGATGACTACCTCCCTGTTATTTATGGAATTA 420  
 Oy 181 TCTTCTGTGGGATTTCCAGGCAATGAGTAGATGATTCACATTTCAATTTCAAAATGA 240  
 Db 421 TCTTCTGTGGGATTTCCAGGCAATGAGTAGATGATTCACATTTCAATTTCAAAATGA 480  
 Oy 241 GACCTGGAAGGACGACATCATATATCTGAACTGCGCTGACAGATGCTGCTATC 300

Db 481 GACCTGGAAGGACGACATCATATATCTGAACTGCGCTGACAGATGCTGCTATC 540  
 Oy 301 TGACCAAGCTCCCTCTCTGATTCAGTATGATGACAGTAGGAGCAAACTGATCTTGGAG 360  
 Db 541 TGACCAAGCTCCCTCTCTGATTCAGTATGATGACAGTAGGAGCAAACTGATCTTGGAG 600  
 Oy 361 ATTTCAATGATGATTTATCCGCTTCAAGCTTCAATTTCAACCTGTATAGAGATCTCT 420  
 Db 601 ATTTCAATGATGATTTATCCGCTTCAAGCTTCAATTTCAACCTGTATAGAGATCTCT 660  
 Oy 421 TCTCACTGTTTCAAGATCTCCGCTACCTGTGTATGATTCACCAATAGAGCTCTTTT 480  
 Db 661 TCTCACTGTTTCAAGATCTCCGCTACCTGTGTATGATTCACCAATAGAGCTCTTTT 720  
 Oy 481 CCATTCACAAAATCGATGATGAGTGTAGCTGTGCTGTGTGTGTGTGTGTGTGTGTGT 540  
 Db 721 CCATTCACAAAATCGATGATGAGTGTAGCTGTGCTGTGTGTGTGTGTGTGTGTGTGT 780  
 Oy 541 TACCTGTCTATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600  
 Db 781 TACCTGTCTATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840  
 Oy 601 GTCTGACCTGACAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 660  
 Db 841 GTCTGACCTGACAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 900  
 Oy 661 CTGCAACTACTTTCTGCTCCCTGCTGATGATGATGATGATGATGATGATGATGATGATG 720  
 Db 901 CTGCAACTACTTTCTGCTCCCTGCTGATGATGATGATGATGATGATGATGATGATGATG 960  
 Oy 721 AACTCTGACCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780  
 Db 961 AACTCTGACCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020  
 Oy 781 CCATTCGCTACTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840  
 Db 1021 CCATTCGCTACTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080  
 Oy 841 TTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900  
 Db 1081 TTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140  
 Oy 901 CTTCATGCTTTCTGACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960  
 Db 1141 CTTCATGCTTTCTGACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200  
 Oy 961 TGGTGTGACGCAAACTTTAGAGAGGCTGTCTCTCAACAGTAGAGTAGCAAGTAAAGCG 1020  
 Db 1201 TGGTGTGACGCAAACTTTAGAGAGGCTGTCTCTCAACAGTAGAGTAGCAAGTAAAGCG 1260  
 Oy 1021 GGAACCTTGAGCAAGCAAGAAATTAAGTAACTCAAAACAACTTTGAATATTTCAATTA 1080  
 Db 1261 GGAACCTTGAGCAAGCAAGAAATTAAGTAACTCAAAACAACTTTGAATATTTCAATTA 1320  
 Oy 1081 C 1081  
 Db 1321 C 1321

RESULT 11  
 US-60-261-974-40  
 ; Sequence 40, Application US/60261974  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Beasley, Ellen  
 ; TITLE OF INVENTION: ISOLATED HUMAN NUCLEAR HORMONE RECEPTOR  
 ; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN NUCLEAR  
 ; TITLE OF INVENTION: HORMONE RECEPTOR PROTEINS, AND USES THEREOF  
 ; FILE REFERENCE: C1001096-PROV  
 ; CURRENT APPLICATION NUMBER: US/60/261,974  
 ; NUMBER OF SEQ ID NOS: 237  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 40

Db 3908 TAGCTGTCATCCGATGACCTTCTTGATGACATCAACAGAGACCAACAGATCGACCT 3967  
 Oy 601 GTCGACCTGACGAGTGGATGAACTGAATATTAATGAGTGAACCTGATTTGA 660  
 Db 3368 GTCTGACCTGACGAGTGGATGAACTGAATATTAATGAGTGAACCTGATTTGA 4027  
 Oy 661 CTGCAACTACTTCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 720  
 Db 4028 CTGCAACTACTTCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 4087  
 Oy 721 AACTGTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 779  
 Db 4088 AACTGTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 4147  
 Oy 780 AACTGTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 839  
 Db 4148 AACTGTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 4207  
 Oy 840 AACTGTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 899  
 Db 4208 AACTGTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 4267  
 Oy 900 GCTTACATGCTTCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 959  
 Db 4268 GCTTACATGCTTCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 4327  
 Oy 960 GCTTACATGCTTCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 1019  
 Db 4328 GCTTACATGCTTCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 4387  
 Oy 1020 GGGAACTTGAAGCAAGAAATTAATGTTACTCAACACCTTGAATATTTGATT 1079  
 Db 4388 GGGAACTTGAAGCAAGAAATTAATGTTACTCAACACCTTGAATATTTGATT 4447  
 Oy 1080 AC 1081  
 Db 4448 AC 4449

RESULT 13  
 US-60-205-423-234  
 ; Sequence 234, Application US/60205423  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Beasley, Ellen  
 ; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED  
 ; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR  
 ; FILE REFERENCE: C1000563  
 ; CURRENT APPLICATION NUMBER: US/60/205,423  
 ; NUMBER OF SEQ ID NOS: 494  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 234  
 ; LENGTH: 8161  
 ; TYPE: DNA  
 ; ORGANISM: HUMAN  
 ; US-60-205-423-234

Query Match 98.8%; Score 1068.4; DB 64; Length 8161;  
 Best Local Similarity 99.8%; Pred. No. 1.9e-295;  
 Matches 1080; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Oy 1 CAAATGCAAACTGAACTCTCTGTTTCTTGCAAGTGAAGAGACCAACATGATG 60  
 Db 3368 CAAATGCAAACTGAACTCTCTGTTTCTTGCAAGTGAAGAGACCAACATGATG 3427  
 Oy 61 AGCACTAGACTATTTAGCAAAATGCTGTATTTCCCGATTAGAGAGCTGTTTGA 120  
 Db 3428 AGCACTAGACTATTTAGCAAAATGCTGTATTTCCCGATTAGAGAGCTGTTTGA 3487  
 Oy 121 ATTGACGTATGAAACATCCCACTCAAGATGACTACCTCCCGTTATTTATGCA 180

Db 3488 ATTGACGTATGAAACATCCCACTCAAGATGACTACCTCCCGTTATTTATGCA 3547  
 Oy 181 TCTTCTGCTGGGATTTCCAGGCAATGACATGATGATTCATTTCAATTTGAAATGA 240  
 Db 3548 TCTTCTGCTGGGATTTCCAGGCAATGACATGATGATTCATTTCAATTTGAAATGA 3607  
 Oy 241 GACCTTGAAGAGCAACATCATTAATGCTGAACCTGACCTGACAGATCTGATTC 300  
 Db 3608 GACCTTGAAGAGCAACATCATTAATGCTGAACCTGACCTGACAGATCTGATTC 3667  
 Oy 301 TGACAGAGCTCCCTTCCGATTTCACTATAGCCAGTGGCCGAAACCTGATTTGGAG 360  
 Db 3668 TGACAGAGCTCCCTTCCGATTTCACTATAGCCAGTGGCCGAAACCTGATTTGGAG 3727  
 Oy 361 ATTGATGATGATGATTTATTCGCTTCACTTCAATTTCAACCTGATTTAGACATTC 420  
 Db 3728 ATTGATGATGATGATTTATTCGCTTCACTTCAATTTCAACCTGATTTAGACATTC 3787  
 Oy 421 TCTTCACTGTTTCAAGCATTTTCGCTTCACTGATGATTCATTCACCAATGACCTGTTT 480  
 Db 3788 TCTTCACTGTTTCAAGCATTTTCGCTTCACTGATGATTCATTCACCAATGACCTGTTT 3847  
 Oy 481 CCATTCAAAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540  
 Db 3848 CCATTCAAAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3907  
 Oy 541 TAGCTGATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600  
 Db 3908 TAGCTGATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3967  
 Oy 601 GTCTGACCTGACCAAGTGGATGAACTCAATATTAATGATGAAACCTGATTTGA 660  
 Db 3968 GTCTGACCTGACCAAGTGGATGAACTCAATATTAATGATGAAACCTGATTTGA 4027  
 Oy 661 CTGCAACTACTTCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 720  
 Db 4028 CTGCAACTACTTCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 4087  
 Oy 721 AACTGTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 779  
 Db 4088 AACTGTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 4147  
 Oy 780 AACTGTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 839  
 Db 4148 AACTGTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 4207  
 Oy 840 AACTGTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 899  
 Db 4208 AACTGTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 4267  
 Oy 900 GCTTACATGCTTCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 959  
 Db 4268 GCTTACATGCTTCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 4327  
 Oy 960 GCTTACATGCTTCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 1019  
 Db 4328 GCTTACATGCTTCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 4387  
 Oy 1020 GGGAACTTGAAGCAAGAAATTAATGTTACTCAACACCTTGAATATTTGATT 1079  
 Db 4388 GGGAACTTGAAGCAAGAAATTAATGTTACTCAACACCTTGAATATTTGATT 4447  
 Oy 1080 AC 1081  
 Db 4448 AC 4449

RESULT 14  
 US-60-205-423-235  
 ; Sequence 235, Application US/60205423  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Beasley, Ellen  
 ; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED



```

Db 3788 TCCCTCAGCTGTTGAGCATCTTCGCTACTGTGTGATCATTCACCCATGAGCTGCTTTT 3847
Qy 481 CCATTCAAAAAGTGCATGTGCAAGTGTAGCTGTGTGTGTGTGATCATTTCACTGG 540
Db 3848 CCATTCAAAAAGTGCATGTGCAAGTGTAGCTGTGTGTGTGTGATCATTTCACTGG 3907
Qy 541 TAGCTGTATTCGATGAGCATCTTGTATCATCAACCAAGAGACCAAGATCAAGCTT 600
Db 3908 TAGCTGTATTCGATGAGCATCTTGTATCATCAACCAAGAGACCAAGATCAAGCTT 3967
Qy 601 GTCTGAGCTCAGCAGTGTGATGATCAATCTATTTAAGTGTCAACCTGATTTTGA 660
Db 3968 GTCTGAGCTCAGCAGTGTGATGATCAATCTATTTAAGTGTCAACCTGATTTTGA 4027
Qy 661 CTGCACTACTTCTTGTGCTTCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Db 4028 CTGCACTACTTCTTGTGCTTCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4087
Qy 721 ACACCTGAGCCATGAGATGAGCTGCAAACTGACAGCTG-CTTAAAGCAGAAAGCAGAGCTA 779
Db 4088 AACCTGAGCCATGAGATGAGCTGCAAACTGACAGCTGCTTAAAGCAGAAAGCAGAGCTA 4147
Qy 780 ACCATTCTGCTACTCTTGTGATTTTACGATGTTTTTTTACCCTTCATATCTTGAAGGTC 839
Db 4148 ACCATTCTGCTACTCTTGTGATTTTACGATGTTTTTTTACCCTTCATATCTTGAAGGTC 4207
Qy 840 ATTGGATGGAATCTGGCTGTTCATCAATCAAGTGTTCATGAGATGAGATGAGATGAA 899
Db 4208 ATTGGATGGAATCTGGCTGTTCATCAATCAAGTGTTCATGAGATGAGATGAGATGAA 4267
Qy 900 GCTTACATCGTTTCTAAGCATGAGTGTGCTGTGAACACCTTGTGTACCTGTACTATAT 959
Db 4268 GCTTACATCGTTTCTAAGCATGAGTGTGCTGTGAACACCTTGTGTACCTGTACTATAT 4327
Qy 960 GTGGTGTGAGCAGCAACTTTCAGAGGCTGTGTCTCAACAGTGTGATGCAAGTAAGC 1019
Db 4328 GTGGTGTGAGCAGCAACTTTCAGAGGCTGTGTCTCAACAGTGTGATGCAAGTAAGC 4387
Qy 1020 GGGAACTTGTAGCAAGCAAGAAATTAAGTACTCAACCAACCTTGAATATTTGATTT 1079
Db 4388 GGGAACTTGTAGCAAGCAAGAAATTAAGTACTCAACCAACCTTGAATATTTGATTT 4447
Qy 1080 AC 1081
Db 4448 AC 4449

```

Search completed: January 30, 2003, 09:39:16  
 Job time : 3519 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 06:06:20 ; Search time 872 Seconds  
(without alignments)  
1406.854 Million cell updates/sec

Title: US-10-010-568-1  
Perfect score: 1081  
Sequence: 1 catatgccaaactgaactc.....ccttgaataattcattac 1081

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapept 1.0

Searched: 2475311 seqs, 567426730 residues

Total number of hits satisfying chosen parameters: 4950622

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents NA New.\*  
1: /cgn2\_6/prodata/1/pna/PCT\_NEW\_COMB.seq.\*  
2: /cgn2\_6/prodata/1/pna/US06\_NEW\_COMB.seq.\*  
3: /cgn2\_6/prodata/1/pna/US07\_NEW\_COMB.seq.\*  
4: /cgn2\_6/prodata/1/pna/US08\_NEW\_COMB.seq.\*  
5: /cgn2\_6/prodata/1/pna/US09\_NEW\_COMB.seq.\*  
6: /cgn2\_6/prodata/1/pna/US10\_NEW\_COMB.seq.\*  
7: /cgn2\_6/prodata/1/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1081	100.0	1414	6	US-10-017-161-525
2	1081	100.0	9905	6	US-10-270-144-3
3	1014	93.8	1014	6	US-10-270-144-3
4	1014	93.8	1014	6	US-10-188-405-7
5	1014	93.8	1014	6	US-10-321-807-27
6	1012.4	93.7	1014	6	US-10-278-141-10
7	1012.4	93.7	1014	6	US-10-278-107-33
8	1012.4	93.7	1014	6	US-10-296-081-10
9	479.8	44.4	545	6	US-10-276-774-102
10	134.4	12.4	1428	6	US-10-270-857-1
11	134.4	12.4	1428	6	US-10-270-587-1
12	134.2	12.4	3055	6	US-10-305-720-1456
13	131.2	12.1	1005	6	US-10-272-983-35
14	131.2	12.1	1436	6	US-10-264-237-1352
15	131.2	12.1	1442	6	US-10-311-671-20
16	123	11.4	1429	6	US-10-305-720-1068
17	107.8	10.0	2025	5	US-09-814-915A-74
18	107.8	10.0	2025	5	US-10-305-720-1482
19	100	9.3	984	5	US-09-461-436B-41
20	97.4	9.0	1571	6	US-10-305-720-1108
21	95.8	8.9	984	5	US-09-461-436B-57
22	94.4	8.7	1428	6	US-10-152-319A-2045
23	93.6	8.7	1041	6	US-10-278-107-35
24	93.6	8.7	1041	6	US-10-321-807-13
25	93.6	8.7	1041	6	US-10-321-807-87
26	93.6	8.7	2807	5	US-09-879-603A-1

27	93.6	8.7	2807	5	US-09-979-603-1	Sequence 1, Appli
28	90.8	8.4	1900	6	US-10-305-720-1484	Sequence 1464, Ap
29	90.8	8.4	2070	1	PCT-US02-29560-44	Sequence 44, Appl
30	90.8	8.4	2070	6	US-10-245-882-44	Sequence 2068, Ap
31	90.4	8.4	1922	6	US-10-152-319A-2068	Sequence 511, App
32	87.6	8.1	1092	6	US-10-321-807-35	Sequence 765, App
33	87.6	8.1	1192	6	US-10-017-161-511	Sequence 807, App
34	87.6	8.1	5015	6	US-10-017-161-765	Sequence 9205, Ap
35	87.6	8.1	8367	6	US-10-017-161-807	Sequence 1, Appli
36	87.2	8.1	2409	5	US-09-360-482B-21	Sequence 19, Appl
37	84	7.8	1059	6	PCT-US02-29560-46	
38	84	7.8	1059	6	US-10-245-882-46	
39	84	7.8	1225	7	US-10-305-720-1235	
40	84	7.8	1670	7	US-60-427-982-317	
41	84	7.8	1679	1	PCT-US02-04915-80	
42	84	7.8	1679	6	US-10-170-385-332	
43	84	7.8	1679	6	US-10-325-899-9205	
44	83.8	7.8	1451	5	US-09-958-805A-1	
45	83.8	7.8	1451	5	US-09-360-482B-19	

## ALIGNMENTS

RESULT 1  
US-10-017-161-525  
Sequence 525, Application US/10017161  
GENERAL INFORMATION:

APPLICANT: SUMA, MAKIKO  
APPLICANT: ASAI, KIYOSHI  
APPLICANT: AKIYAMA, YUTAKA  
APPLICANT: ASURAYANT, HIROYUKI  
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS  
FILE REFERENCE: 084335/0152  
CURRENT APPLICATION NUMBER: US/10/017, 161  
PRIOR APPLICATION NUMBER: 2002-12-18  
PRIOR FILING DATE: 2001/246789  
NUMBER OF SEQ ID NOS: 2430  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 525  
LENGTH: 1414  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: source  
LOCATION: (1)..(1414)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (201)..(1214)  
US-10-017-161-525

Query Match 100.0%; Score 1081; DB 6; Length 1414;  
Best Local Similarity 100.0%; Pred. No. 8.4e-295;  
Matches 1081; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CATATGCCAACTGAACCTCTGTTTCTGGAAGATGAAGAGAACCAACCATGATG	60
DB	148	CATATGCCAACTGAACCTCTGTTTCTGGAAGATGAAGAGAACCAACCATGATG	207
QY	61	AGGCACATGACTATTTAGCAAAATGCTTCTGATTTCCCGATTTATGACAGTCTTTGGAA	120
DB	208	AGGCACATGACTATTTAGCAAAATGCTTCTGATTTCCCGATTTATGACAGTCTTTGGAA	267
QY	121	ATTGCACTATGAAATCATCTCCACTCAAGTGAAGTCACTTCCCTGTTATTTATGACATTA	180
DB	268	ATTGCACTATGAAATCATCTCCACTCAAGTGAAGTCACTTCCCTGTTATTTATGACATTA	327
QY	181	TCTTCCTCGGGATTTCCAGGAGTGAAGTGAATGATTCATTCATTTCAAAATGA	240
DB	328	TCTTCCTCGGGATTTCCAGGAGTGAAGTGAATGATTCATTCATTTCAAAATGA	387
QY	241	GACCTTGAAGACACACATCATTTATGCTGAACCTGCGCTGCACAGATCTGCTATTC	300

Db 9156 CTACACGCTTTCTAGACCATTTAGCTGCTCTGAAACCTTTGGTAACCTGTTACTATATG 9215  
 Qy 961 TGGTGTGACGACCACTTTGAGAGGCTGTCTGTAAACGTAGATGCAAGTAAGCG 1020  
 Db 9216 TGGTGTGACGACCACTTTGAGAGGCTGTCTGTAAACGTAGATGCAAGTAAGCG 9275  
 Qy 1021 GGAACCTTGACGACCAAGAAATTTAGTTACTGAAACCACTTTGAAATTTTCAATTA 1080  
 Db 9276 GGAACCTTGACGACCAAGAAATTTAGTTACTGAAACCACTTTGAAATTTTCAATTA 9335  
 Qy 1081 C 1081  
 Db 9336 C 9336

## RESULT 3

US-10-270-144-1  
 ; Sequence 1, Application US/10270144  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MEI, Ming-Hui et al  
 ; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED  
 ; TITLE OF INVENTION: RECEPTORS, NOCLEIC ACID MOLECULES ENCODING HUMAN GPCR  
 ; FILE REFERENCE: CL000750CON  
 ; CURRENT APPLICATION NUMBER: US/10/270,144  
 ; PRIOR FILING DATE: 2002-10-15  
 ; PRIOR APPLICATION NUMBER: 60/205,196  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1014  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-10-270-144-1

Query Match 93.8%; Score 1014; DB 6; Length 1014;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-276;

Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 ATGAATGAGCCACTAGACTATTGAGCAATGCTTGTGATTTCCCGCATTAAGAGCGCT 113  
 Db 1 ATGAATGAGCCACTAGACTATTGAGCAATGCTTGTGATTTCCCGCATTAAGAGCGCT 60  
 Qy 114 TTGGAATTTGACGTGATGAAACATCCCACTCAAGATGACACTACCTCCCTGTTATTTAT 173  
 Db 61 TTGGAATTTGACGTGATGAAACATCCCACTCAAGATGACACTACCTCCCTGTTATTTAT 120  
 Qy 174 GGCATTATTTCTCTGTGGATTTTCAAGCAATGCAAGTATGATTCACATTTTC 233  
 Db 121 GGCATTATTTCTCTGTGGATTTTCAAGCAATGCAAGTATGATTCACATTTTC 180  
 Qy 234 AAAATGAGACTTGAAGAGCAGCACCATCATATATGCTGAACTGGCGCTGCAAGATCTG 233  
 Db 181 AAAATGAGACTTGAAGAGCAGCACCATCATATATGCTGAACTGGCGCTGCAAGATCTG 240  
 Qy 234 CTGATCTGACAGCCTCCCTCTCTGATTCATCTATGCGAGTGGCGAAACTGAGATC 353  
 Db 241 CTGATCTGACAGCCTCCCTCTCTGATTCATCTATGCGAGTGGCGAAACTGAGATC 300  
 Qy 354 TTTGAGATTTTATGTTAGTTATTCGCTTCAAGCTTTCATTTCAACCTGATATAGCAG 413  
 Db 301 TTTGAGATTTTATGTTAGTTATTCGCTTCAAGCTTTCATTTCAACCTGATATAGCAG 360  
 Qy 414 ATCCCTTCTCAGCAGCTTTGAGCACTCCGCTAGTGTATATTTTCAACCAATGAGC 473  
 Db 361 ATCCCTTCTCAGCAGCTTTGAGCACTCCGCTAGTGTATATTTTCAACCAATGAGC 420  
 Qy 474 TGCCTTTTCCATTCACAAAACGATGTGAGTGTAGCCGCTGTGTGTGTGTGTGTGTGT 533  
 Db 421 TGCCTTTTCCATTCACAAAACGATGTGAGTGTGTAGCCGCTGTGTGTGTGTGTGTGTGT 480

Qy 534 TCACGTGAGCTGTGATTTCCGATGAGACTTCTTGTATCATATCAACCAAGGACCAACAGA 593  
 Db 481 TCACGTGAGCTGTGATTTCCGATGAGACTTCTTGTATCATATCAACCAAGGACCAACAGA 540  
 Qy 594 TCACGTGAGCTGTGATTTCCGATGAGACTTCTTGTATCATATCAACCAAGGACCAACAGA 653  
 Db 541 TCACGTGAGCTGTGATTTCCGATGAGACTTCTTGTATCATATCAACCAAGGACCAACAGA 600  
 Qy 654 ATTTGACGTGACACTTCTTCTGCTCCCTGCTGTGTATGATGACACTTTGTATACAGC 713  
 Db 601 ATTTGACGTGACACTTCTTCTGCTCCCTGCTGTGTATGATGACACTTTGTATACAGC 660  
 Qy 714 ATTATCCACTGACCTGACCACTGACGAACTGAACTGACAGCTGCTTAAAGCAAGAAAGCA 773  
 Db 661 ATTATCCACTGACCTGACCACTGACGAACTGAACTGACAGCTGCTTAAAGCAAGAAAGCA 720  
 Qy 774 AGGCTAACCAATTCGCTACTCTGCTGATTTTACGTAATTTTACCTTCCATATCTTG 833  
 Db 721 AGGCTAACCAATTCGCTACTCTGCTGATTTTACGTAATTTTACCTTCCATATCTTG 780  
 Qy 834 AGGCTAACCAATTCGCTACTCTGCTGATTTTACGTAATTTTACCTTCCATATCTTG 893  
 Db 781 AGGCTAACCAATTCGCTACTCTGCTGATTTTACGTAATTTTACCTTCCATATCTTG 840  
 Qy 894 CATGACCTTACATGCTTTTCTTAAACATTAAGCTGCTGAAACACTTGTGTAACTGTTA 953  
 Db 841 CATGACCTTACATGCTTTTCTTAAACATTAAGCTGCTGAAACACTTGTGTAACTGTTA 900  
 Qy 954 CTATATGCTGTGTGACGCGCAACTTTTACAGAGCTGTCTGCTGAACTGATGATGCAAA 1013  
 Db 901 CTATATGCTGTGTGACGCGCAACTTTTACAGAGCTGTCTGCTGAACTGATGATGCAAA 960  
 Qy 1014 GTAAGCGGAACTTGAAGCAAGAAATTTAGTTACTCAAAACACCTTGA 1067  
 Db 961 GTAAGCGGAACTTGAAGCAAGAAATTTAGTTACTCAAAACACCTTGA 1014

## RESULT 4

US-10-188-405-7  
 ; Sequence 7, Application US/10188405

; GENERAL INFORMATION:  
 ; APPLICANT: Tian, Hui  
 ; APPLICANT: Dai, Kang  
 ; APPLICANT: Chen, Jin-Long  
 ; APPLICANT: Zhao, Jiaqiang  
 ; APPLICANT: Cutler, Gene  
 ; APPLICANT: Tularik Inc.  
 ; TITLE OF INVENTION: Novel Receptors  
 ; FILE REFERENCE: 018781-008410US  
 ; CURRENT APPLICATION NUMBER: US/10/188,405  
 ; PRIOR FILING DATE: 2002-07-01  
 ; PRIOR APPLICATION NUMBER: US 60/302,800  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 7  
 ; LENGTH: 1014  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: human TGR164  
 US-10-188-405-7

Query Match 93.8%; Score 1014; DB 6; Length 1014;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-276;

Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 ATGAATGAGCCACTAGACTATTGAGCAATGCTTGTGATTTCCCGCATTAAGAGCGCT 113  
 Db 1 ATGAATGAGCCACTAGACTATTGAGCAATGCTTGTGATTTCCCGCATTAAGAGCGCT 60  
 Qy 114 TTGGAATTTGACGTGATGAAACATCCCACTCAAGATGACACTACCTCCCTGTTATTTAT 173

```
Db 541 TCACCTGTCTGACCTGACCACTTGGATGAACTCAATTAATTAAGTGAACCTG 600
Qy 654 ATTTGACTGCACTACTTTTCTGCTCCCTTGGATAGTGAACCTTGTATACGAC 713
Db 601 ATTTGACTGCACTACTTTTCTGCTCCCTTGGATAGTGAACCTTGTATACGAC 660
Qy 714 ATTTGCACTGCACTACTTTTCTGCTCCCTTGGATAGTGAACCTTGTATACGAC 773
Db 661 ATTTGCACTGCACTACTTTTCTGCTCCCTTGGATAGTGAACCTTGTATACGAC 720
Qy 774 AGGCTAACCAATTCCTGCTACTCTTGCATTTTACGATTTTTCACCTTCCATATCTTG 833
Db 721 AGGCTAACCAATTCCTGCTACTCTTGCATTTTACGATTTTTCACCTTCCATATCTTG 780
Qy 834 AGGCTAACCAATTCCTGCTACTCTTGCATTTTACGATTTTTCACCTTCCATATCTTG 893
Db 781 AGGCTAACCAATTCCTGCTACTCTTGCATTTTACGATTTTTCACCTTCCATATCTTG 840
Qy 894 CATGAAGCTTACATCCGTTTTCAGCACTTACGATTTTTCACCTTCCATATCTTG 953
Db 841 CATGAAGCTTACATCCGTTTTCAGCACTTACGATTTTTCACCTTCCATATCTTG 900
Qy 954 CATATAGTGTGTGTCAGCACTTACGATTTTTCACCTTCCATATCTTG 1013
Db 901 CATATAGTGTGTGTCAGCACTTACGATTTTTCACCTTCCATATCTTG 960
Qy 1014 GTAAAGGGGAACTTGAAGCAAGAAAGAAATTTACTCAACCAACCTTGA 1067
Db 961 GTAAAGGGGAACTTGAAGCAAGAAAGAAATTTACTCAACCAACCTTGA 1014
```

## RESULT 6

US-10-278-141-10  
Sequence 10, Application US/10278141

## GENERAL INFORMATION:

APPLICANT: PATERSON, Chandra  
APPLICANT: LU, Dyrung Aina M.  
APPLICANT: THORNTON, Michael  
APPLICANT: LU, Yan  
APPLICANT: TRIBOULEY, Catherine M.  
APPLICANT: GRAUL, Richard  
APPLICANT: KHAN, Farrah A.  
APPLICANT: GANDHI, Ameena R.  
APPLICANT: WALIA, Narinder K.  
APPLICANT: NGUYEN, Daniel B.  
APPLICANT: YUE, Henry  
APPLICANT: HARALIA, April  
APPLICANT: ELLIOTT, Vicki S.  
APPLICANT: LAL, Preeti  
APPLICANT: REDDY, Roopa  
APPLICANT: KALLICK, Deborah A.  
APPLICANT: TANG, Y. Tom  
APPLICANT: AU-YOUNG, Janice  
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS  
FILE REFERENCE: PI-0096 USA  
CURRENT APPLICATION NUMBER: US/10/278,141  
PRIOR FILING DATE: 2002-10-21  
PRIOR APPLICATION NUMBER: 60/208,834  
PRIOR FILING DATE: 2000-06-02  
PRIOR APPLICATION NUMBER: 60/207,566  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: US01/16285  
PRIOR FILING DATE: 2001-05-17  
PRIOR APPLICATION NUMBER: 60/205,628  
PRIOR FILING DATE: 2000-05-18  
PRIOR APPLICATION NUMBER: 60/208,861  
PRIOR FILING DATE: 2000-06-02  
PRIOR APPLICATION NUMBER: 60/206,222  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PERL Program  
SEQ ID NO 10  
LENGTH: 1014

TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Inctye ID No: 6575963CH1  
US-10-278-141-10

Query Match 93.7%; Score 1012.4; DB 6; Length 1014;  
Best Local Similarity 99.9%; Pred. No. 1.7e-275;  
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy 54 ATGAATGAGCACTGATGATTTTATGCAATGCTTTGATTTTCCGATTAAGCTGCT 113
Db 1 ATGAATGAGCACTGATGATTTTATGCAATGCTTTGATTTTCCGATTAAGCTGCT 60
Qy 114 TTGGAAATTCACATGATGAAGAAATCCACCTGAAAGCACTACTCCCTTTATTTAT 173
Db 61 TTGGAAATTCACATGATGAAGAAATCCACCTGAAAGCACTACTCCCTTTATTTAT 120
Qy 174 GGCATTAATCTTCTCGTGGGATTTCCAGGCAATGCAAGATGATATCACTTACATTTTC 233
Db 121 GGCATTAATCTTCTCGTGGGATTTCCAGGCAATGCAAGATGATATCACTTACATTTTC 180
Qy 234 AAATGAGACTTGGAAAGAGAGACCAATCATTAATGCTGAACCTGCGCTGCAAGATCTG 293
Db 181 AAATGAGACTTGGAAAGAGAGACCAATCATTAATGCTGAACCTGCGCTGCAAGATCTG 240
Qy 294 CTGATCTGACCAAGCCCTCCCTCCGATTTCACTATGCACTGCAAGTGGGAAACTGATC 353
Db 241 CTGATCTGACCAAGCCCTCCCTCCGATTTCACTATGCACTGCAAGTGGGAAACTGATC 300
Qy 354 TTGGAGATTTCAATGATGATTAATCGCTTCACTGCTTCACTTCAACCTGATATGACG 413
Db 301 TTGGAGATTTCAATGATGATTAATCGCTTCACTGCTTCACTTCAACCTGATATGACG 360
Qy 414 ATCTCTTCTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCT 473
Db 361 ATCTCTTCTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCT 420
Qy 474 TGCCTTTCATTCAGAAATCGATGATGATGATGATGATGATGATGATGATGATGATG 533
Db 421 TGCCTTTCATTCAGAAATCGATGATGATGATGATGATGATGATGATGATGATGATG 480
Qy 534 TCACCTGTGCTGACCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 593
Db 481 TCACCTGTGCTGACCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Qy 594 TCACCTGTGCTGACCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 653
Db 541 TCACCTGTGCTGACCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Qy 654 ATTTGACTGCACTACTTTTCTGCTCCCTTGGATAGTGAACCTTGTATACGAC 713
Db 601 ATTTGACTGCACTACTTTTCTGCTCCCTTGGATAGTGAACCTTGTATACGAC 660
Qy 714 ATTTGCACTGCACTACTTTTCTGCTCCCTTGGATAGTGAACCTTGTATACGAC 773
Db 661 ATTTGCACTGCACTACTTTTCTGCTCCCTTGGATAGTGAACCTTGTATACGAC 720
Qy 774 AGGCTAACCAATTCCTGCTACTCTTGCATTTTACGATTTTTCACCTTCCATATCTTG 833
Db 721 AGGCTAACCAATTCCTGCTACTCTTGCATTTTACGATTTTTCACCTTCCATATCTTG 780
Qy 834 AGGCTAACCAATTCCTGCTACTCTTGCATTTTACGATTTTTCACCTTCCATATCTTG 893
Db 781 AGGCTAACCAATTCCTGCTACTCTTGCATTTTACGATTTTTCACCTTCCATATCTTG 840
Qy 894 CATGAAGCTTACATCCGTTTTCAGCACTTACGATTTTTCACCTTCCATATCTTG 953
Db 841 CATGAAGCTTACATCCGTTTTCAGCACTTACGATTTTTCACCTTCCATATCTTG 900
Qy 954 CATATAGTGTGTGTCAGCACTTACGATTTTTCACCTTCCATATCTTG 1013
```

QY 54 ATGAATGAGCAGCTAGACCTATTGAGCAAAAGCTTCTGATTTTCCCGATTATGACACTGCT 113  
 Db 1 ATGAATGAGCAGCTAGACCTATTGAGCAAAAGCTTCTGATTTTCCCGATTATGAGCACTGCT 60  
 QY 114 TTGGAATTTGCACTGATGAAAAATCCCACTCAAGATGACCTACCTCCCTGTTATTTAT 173  
 Db 61 TTTGAAATTTGCACTGATGAAAAATCCCACTCAAGATGACCTACCTCCCTGTTATTTAT 120  
 QY 174 GGCATTATTTCTCTCGTGGATTTTCCAGGCAATGCACTAGATGATTCACACTTAATTTTC 233  
 Db 121 GGCATTATTTCTCTCGTGGATTTTCCAGGCAATGCACTAGATGATTCACACTTAATTTTC 180  
 QY 234 AAAATGAGACCTTGGAAAGCAGCACCATCATTAATGCTGAACTGGCTGCAAGATCTG 293  
 Db 181 AAAATGAGACCTTGGAAAGCAGCACCATCATTAATGCTGAACTGGCTGCAAGATCTG 240  
 QY 294 CTGATCTGACAGCAGCTCCCTCTCCGATTCACTATATCCAGTGGCGAAAACTGGATC 353  
 Db 241 CTGATCTGACAGCAGCTCCCTCTCCGATTCACTATATCCAGTGGCGAAAACTGGATC 300  
 QY 354 TTGGAATTTCAATGTTGAATTATACCGCTCAGCTTCATTCAACCTGTTATGAGAC 413  
 Db 301 TTGGAATTTCAATGTTGAATTATACCGCTCAGCTTCATTCAACCTGTTATGAGAC 360  
 QY 414 ATCTCTTCCCACTGTTTTCAGACTCTTCCGCTACCTGTGTATCATTCACCAATGAGC 473  
 Db 361 ATCTCTTCCCACTGTTTTCAGACTCTTCCGCTACCTGTGTATCATTCACCAATGAGC 420  
 QY 474 TGTCTTCCATTCAAAACCTGATGTGCACTGTGTAAGCTGTGTGTGTGTGATCATTT 533  
 Db 421 TGTCTTCCATTCAAAACCTGATGTGCACTGTGTAAGCTGTGTGTGTGTGATCATTT 480  
 QY 534 TCACTGGTAGCTGTCATTTCCGATGACCTTTTGATCACAATCAACCAAGACCAACAGA 593  
 Db 481 TCACTGGTAGCTGTCATTTCCGATGACCTTTTGATCACAATCAACCAAGACCAACAGA 540  
 QY 594 TCAGCTGTCTGCACCTCACAGTTGGATGAACTCATTAATTAAGGTGACAACTCG 653

```

APPLICANT: Hyseq, Inc.
APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
CURRENT APPLICATION NUMBER: US/10/276,774
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: Custom
SEQ ID NO 102
LENGTH: 545
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(545)
OTHER INFORMATION: n = a,t,c or g
US-10-276-774-102

```

Query Match	44.4%	Score 479.8	DB 6	Length 545
Best Local Similarity	98.7%	Pred. No. 2e-125		
Matches 526	Conservative	0	Mismatches 2	Indels 5
				Gaps 4
QY	265	TTATGCTGAACCTGG-CCTGCACAGATCGTGG-TATCTGACAGAGCTCCCTTCTGAT		322
Db	532	TAATCTGTAACCTGGCCCTGCACAGATCTGCTTATCTGACAGAGCTCCCTTCTGAT		473
QY	323	TCACACTATGCGAGTGGCGGAAAATGGAATCTTTGGAGATTTCATGTGAATTATCCG		382
Db	472	TCACACTATGCGAGTGGCGGAAAATGGAATCTTTGGAGATTTCATGTGAATTATCCG		413
QY	383	CTTGAGCTTCCATTTCACACCTGTATAGAGATCCTCTCTCCACCTGTTTCAGATCTT		442
Db	412	CTTGAGCTTCCATTTCACACCTGTATAGAGATCCTCTCTCCACCTGTTTCAGATCTT		353

```

Db 176 TTTATGGAGTNGAGTTCGTTGGAGACCTTGGAAATACATGTTGTTTACGGCTAC 235
Qy 228 ATTTTCAAAATAGACCTTGGAGAGAGACCATCATATATGCGAACCTGGCTGACA 287
Db 236 ATCTTCTCTGAAAGACTGGAACAGCATTAATTTATCTTTTAACTCTCTGCTCT 295
Qy 288 GATCTGCTGATGACAGCCTCCCTTCCTGATTCATCTACTATGACGAGGGGAAAC 347
Db 296 GACTTACGTTTCTGTCACACCTCCCATGCTATAGAGGATATGCAATG--AAAC 352
Qy 348 TGGATCTTGGAGATTCATATGCTAATAGTTATTCGCTTACGCTTCACTTCAACTGAT 407
Db 353 TGGATATATGAGAGCTGCTGACATAGACACGATATGCTTATATGCAACTCTAT 412
Qy 408 AGCAGCATCTCTCTCTCACTGTTTCAAGATTTCCGCTACTGCTGATCAACCA 467
Db 413 ACCAGCATCTCTCTCTCACTGTTTCAAGATTTCCGCTACTGCTGATCAACCA 472
Qy 468 ATGAGCTGCTTTCATTCACAAAATCGATGAGTGTGAGCCGCTGCTGCTGCTG 527
Db 473 TTTCCGAAACAACCTTCTGCAAAAAGAGTGTGCTATTTTAACTCTTGGCAATG 532
Qy 528 ATCATTTCACTGTAAGCTGTATTCGATGACCTTCTGATCAATCAACGAAGACC 587
Db 533 GTTTTACGATCTTAAAGTACTACCCATCTTCCCTTAAATCCCTGTTAACTGAC 592
Qy 588 AACAGATCAAGCTGCTGACCTGACAGCTTCCGATGAACTCATATATTAAGTGTAC 647
Db 593 AATGGACCACTGTAATGATTTGCAAGTCTGGAAGACCCCACTAACCTCATTTAC 652
Qy 648 AACCTGATTTTGAAGTGAACACTTCTGCTCCCTTGGAGATGATGACCTTGTAT 707
Db 653 AGCATGCTGCTAACACTGTTGGGCTTCTTATTTCTTCTTGTGATGTTGTTCTTAT 712
Qy 708 ACCAGATTT-----ATCCACTCTGACCCCATGAGACTGCAAGTGAAGCTGCTTAT 761
Db 713 TAAAGATGCTCTCTCTTAAAGACAGAAATAGGAGATGCTACGCTGCTCCCTT 772
Qy 762 CAGAAAGCAGAGGCTAACATTTGCTACTCTTGCATTTTAACTGATGTTTAACTCC 821
Db 773 GAAAAGCTCTCAACTGCTGATCATGAGAGTGTATCTTCTGCTGCTTTTACACC 832
Qy 822 TTCCATATTTGAGGCTCATTCGATCGAATCTCGCTGCTTCAATCA-----GTTGT 875
Db 833 TATCAGCTATCGGAATGAGATGCGCTTCAAGCTGGAAGTTGAAGCATATCAG 892
Qy 876 TCCATTTGAGATCAATTCATGAGCTTACATGCTTTCATAGACCATTAAGCTGCTGAC 935
Db 893 TGCATCTAGTGTGATCAACTCTTTTACATTTGACACAGGCTGTGGCTTTTGAAC 952
Qy 936 ACCTTGTAACTGTTACTATATGTTGTTGCTGACGACACTT 979
Db 953 AGTGTATCAACCTGCTCTTCTTATTTTCTTGGGAGATCACTT 996

```

RESULT 12  
 US-10-305-720-1456  
 ; Sequence 1456, Application US/10305720  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.  
 ; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression  
 ; FILE REFERENCE: PA-0002-1-CON  
 ; CURRENT APPLICATION NUMBER: US/10/305,720  
 ; PRIOR FILING DATE: 2002-11-26  
 ; PRIOR APPLICATION NUMBER: 09/016,434  
 ; NUMBER OF SEQ ID NOS: 1490  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 1456  
 ; LENGTH: 3055  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:

```

; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No: 9798835
US-10-305-720-1456
Query Match 12.4%; Score 134.2; DB 6; Length 3055;
Best Local Similarity 50.1%; Pred. No. 1e-27;
Matches 424; Conservative 0; Mismatches 408; Indels 15; Gaps 3;
Qy 145 TCAAGATGCACTACCTCCCTGTTATTTATGAGATTTATCTTCCGTGGAGATTTCCAGCA 204
Db 995 TCCAGTTTACTACTGCGCGCTGTCTACATCTTGTATTCATCATCGGCTTCTCGGCA 1054
Qy 205 ATGCAATGATGATTCATCACTTACATTTTCAAAATGAGACCTTGGAGAGAGACCATCA 264
Db 1055 ACAGCTGGCCATCTGAGATGTTGCTTCCACATGAAAGCCCTGAGAGGATTCGGGT 1114
Qy 265 TTATGCTGAACCTGGCTGACAGATCTGCTGATTTGAACAGCCTCCCTTCTGATTC 324
Db 1115 ACATGTTCAATTTGGCTGCTGCGCACTTCTGATGCTGCTGCTGCAAGCTGATCT 1174
Qy 325 ACTATATGCAAGTGGCGAAACTGGAATCTTGGAGATTTCAATGATTAATTCGGT 384
Db 1175 TCTACTACTTGAATAAACAGCTGATCTTGGGAGTGCATGTTAACTGACAGAGT 1234
Qy 385 TCAAGTTCAATTTCAACTGTATAGACATCTCTCTCACTGCTTTCAGATCTTCC 444
Db 1235 TCATCTTCAATGATGAACCTTAT--GGCATCTGTTCTGACATGATCATGATGCCACC 1291
Qy 445 GCTACTGTGATATTCACCCATGAGCTGCTTTCATTCACAAAATCGATGAG 504
Db 1292 GGTACAGGAGTGTGTGATCCCTCAAGTCCCTGCGGCGCTCAAAAAGATGGA 1351
Qy 505 TTTAGCCTGTGCTGTGTGTGATCATTTCACTGTAAGCTGTATTCGATGACTT-- 562
Db 1352 TCTGTACAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1411
Qy 563 -CTTGAATCAATCAACCAAGAGCAACAGATGAGCTGCTGCACTCAACCTGAG 621
Db 1412 ACTCAGGTACCGGGGTCGCAAAAAGCAAAACATCACTGTTACGACACCACTCAGAG 1471
Qy 622 ATGAATCAATATTTAATGTGTACAACTGATTTTGAATGCACTGCACTTCTGCTCC 681
Db 1472 AGTACCTGCAAGTATTTATCTATCAAGCATGACAGACCGTGGCATGTTCTGTGTC 1531
Qy 682 CTTGTGATATGATGACACTTGTGTATACCACTTATTCACACTGTGACCATGAGTGC 741
Db 1532 CTTGTGCTGATCTTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1591
Qy 742 AAATGACAGCTGCTTAAAGCAAGAAAGCAAGGTTAAACATCTGCTACTGCTGAT 801
Db 1592 TGGACAACTCTCTGTGAGAGAAATGATTTTACCTGTTAATCATTTGATGATGAT 1651
Qy 802 TTATGATATTTTATTTTACCTTTCATATCTGAGGCTCATTCGATGCAATCTGCTG 861
Db 1652 TTGCTGTGCTTCAATCTTTCATGATGATTAATGATTAATGATTAATGATTAAT 1711
Qy 862 TTT-----CAATCACTTGTTCATTTGATGATTCATGATGATGATGATGATGAT 912
Db 1712 ATTTTCAACCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1771
Qy 913 CTAGACATTAAGTGTGCTGAGACCTTGTGTAACCTGTTACTATATGTTGTGCTGAG 972
Db 1772 CAAGAGTCTAGCAAGTCTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1831
Qy 973 ACAACTT 979
Db 1832 ATACTTT 1838

```

RESULT 13  
 US-10-272-983-35  
 ; Sequence 35, Application US/10272983  
 ; GENERAL INFORMATION:

[illegible]

Query Match	12.14;	Score 131.2;	DB 6;	Length 1542;
Best Local Similarity	49.33;	Pred. No. 5.08-27;		
Matches 436;	Conservative 0;	Mismatches 433;	Indels 15;	Gap
Qy 108	GCTGCTTTGGAAATATGACATGATGAAACAATCCCACTCAAGATGACATACCTCCCTGT	1		
Db 222	GCAATTCGCAAAAACCTGCTGGCAGCAGAGGCTGCCCTCGAAAAAGTACTACTTTCATT	2		
Qy 168	ATTATGSCATTATCTTCTCTGGGAAATTCAGGGCAATGCAATGATGATATCACTTAC	2		
Db 282	TTTTATGGGATTTGAGTTGGTTGGGAGCTCTTGGAAATACATTTGTTTTCAGGCTAC	3		
Qy 228	ATTTTCAAAATGAGACCTTGGAAAGAGCAGCACCATCATTAATGCTGAACCTGGCTGCAC	28		
Db 342	ATCTTCTCTCTGGAAGACTGGACAGACGATAAATATTTATCTCTTTAACCTCTCTGTCT	40		
Qy 288	GATCTGCTATCATCGACCGCCCTCCCTCTGATTCACACTACTATGCCAGTGGCAAAAC	34		
Db 402	GACTTACCTTTCTGCGACCCCTCCCACTGCTGATAGAGATTAAGCAATGACCAATG	45		
Qy 348	TGATCTTTGGAGATTCATGTGTAAAGTTTAAACGCTTCAGCTTCATTCAACTCTGAT	40		
Db 459	TGATATATGAGAGAGCTGCTGCAATAGCAACCATATATGCTTCAATGCCAACCTCAT	51		
Qy 408	AGAGAGATCTCTTCTCTCACTGTTTCAGCATCTTCGCTACTGCTGATCATTCACCCA	46		
Db 519	ACCAGATCTCTTCTCACTTTATGAGCATTAATTCATATCTGATTAATTAATGATTCCT	57		
Qy 468	ATGAGCTGCTTTCATTACAAAACTGAGTGTAGCTGTAGCCTGTGCTGTGG	52		
Db 579	TTCCGAGAACCTTCTGCAAAAGAAAGTTGTCTATTTAACTCCTTGGCAATTTGG	63		
Qy 528	ATCATTTCACTGTAGCTGTCAATTCGATGACCTTTTGATCAGATCAACCAAGAGAC	58		
Db 639	GTTTATGTAACCTTAAGATTAACCAATCTCCCTTTAAATCTGTTATTAACGAC	69		
Qy 588	AAAGCATAGCCTGTCTCGACCTGACCAAGTGGGATGAATCAATATCTAATAGTGTAC	64		
Db 659	AATGCAACCACTGTATGATTTTGAAGTTTGGAGACCCCACTACACCTCATTTAC	75		
Qy 648	AACCTGATTTGATGGAATCACTTTCTGCTCCCTTGGTGTATGACACTTGTCTAT	70		
Db 759	AGCATGTCTTAACACTGTTGGGGTTCCTATTTCTCTTTTGTGATGTCTTTTAT	81		

2y 708 ACCGAGAT-----ATCGACACTCTGACCCAGTGAAGTGCAAACTGACAGCTGCCTTAAG 761  
|||  
Db 819 TACAGATGCTCTCTTCTTAAGCAGAGATAGGAGTGTCTACTGCTCTGCCCTT 878  
|||  
2y 762 CAGAAAGCAGAAAGGCTAACCATTCYGTACTCCCTTGCAATTTTAACTATGTTTTTACC 821  
|||  
Db 879 GAAAGCTCTCAACTTGGTATCATGAGCAGTGGTAATCTTCTGTGCTTTTACACC 938  
|||  
2y 822 TTCATATCTTGAGGGTCAATCGAATCGACTGCTCTTCAATCA-----GTGT 875  
|||  
Db 939 TATCAGCTCATGCGGAATGAGATGCTTCAAGCTGCGGAGTTGAGAGAGATCAG 998  
|||  
2y 876 TCCATTGAGATCAGATCCATGAAGCTTACATCGTTTAAACCATTAAGTGCCTGAAC 935  
|||  
Db 999 TGCATCAGGTGCTCATCACTCTTTACATGAGACAGGCTTTGGCTTCTGAAC 1058  
|||  
2y 936 ACCTTGTAACTGTTACTATATGTGAGTCAAGCGCAACTT 979  
|||  
Db 1059 AGTGTCAATCAACCTGTCTTCTATTTCTTTTGGAGATCACTT 1102  
|||

Search completed: January 30, 2003, 07:08:00  
Job time : 916 secs



APPLICANT: Chen, Ruoping  
 APPLICANT: Dang, Hong T.  
 APPLICANT: Liaw, Chen W.  
 APPLICANT: Lin, I-Lin  
 TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors  
 FILE REFERENCE: AREN0050  
 CURRENT APPLICATION NUMBER: US/10/272,983  
 CURRENT FILING DATE: 2002-10-17  
 PRIOR APPLICATION NUMBER: US/09/417,044  
 PRIOR FILING DATE: 1999-10-12  
 PRIOR APPLICATION NUMBER: 60/109,213  
 PRIOR FILING DATE: 1998-11-20  
 PRIOR APPLICATION NUMBER: 60/120,416  
 PRIOR FILING DATE: 1999-02-16  
 PRIOR APPLICATION NUMBER: 60/121,851  
 PRIOR FILING DATE: 1999-02-26  
 PRIOR APPLICATION NUMBER: 60/123,946  
 PRIOR FILING DATE: 1999-03-12  
 PRIOR APPLICATION NUMBER: 60/123,949  
 PRIOR FILING DATE: 1999-03-12  
 PRIOR APPLICATION NUMBER: 60/136,436  
 PRIOR FILING DATE: 1999-05-28  
 PRIOR APPLICATION NUMBER: 60/136,437  
 PRIOR FILING DATE: 1999-05-28  
 PRIOR APPLICATION NUMBER: 60/136,439  
 PRIOR FILING DATE: 1999-05-28  
 PRIOR APPLICATION NUMBER: 60/136,567  
 PRIOR FILING DATE: 1999-05-28  
 Remaining Prior Application data removed - See File Wrapper or PAM.  
 NUMBER OF SEQ ID NOS: 74  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 35  
 LENGTH: 1005  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 JS-10-272-983-35

Query Match 12.1%; Score 131.2; DB 6; Length 1005;  
 Best Local Similarity 49.3%; Pred. No. 5e-27;  
 Matches 436; Conservative 0; Mismatches 433; Indels 15; Gaps 3;  
 108 GCTGCTTTTGGAAATTCAGTGAAGAAATCCCACTCAAGATGACCTGCTGTT 167  
 25 GCACCTTGCAAAACTGCTGGCAGCAGAGCTGCTGAAAGTACTACCTTCCATT 84  
 168 ATTATGCGATTATCTCTCTGCGGAAATTCAGGCAATGAGTAGATATTCACCTTAC 227  
 85 TTTATATGGAATGAGTGGTCTGTTGGAGTCTTGAAATACCATTTGTTTACGGCTAC 144  
 228 ATTTTCAAAATGAGACCTTGGAGAGCAGCAGCATATTATGCTGAACCTGGCGGACA 287  
 145 ATCTCTCTCTGGAAGAACTGGAACGAGATATTTATCTTTAACTCTCTGCTCT 204  
 288 GATCTGCTGATATGACCAAGCTCCCTTCTGATTCATACTATGCGAGTGGGAAAC 347  
 205 GACTTACCTTTTCTGACACCTCCCATGCTGATTAAGAGTTATGCAAGG---AAAC 261  
 348 TGGATCTTTGAGATTTCATGTTGAATTATCCGCTTCACTTCACTTCACTGAT 407  
 262 TGGATATATGAGAGCGTCTCTGATTAAGAACGATATGCTTTCATGCAACCTCTAT 321  
 408 AGAGCATCTCTCTCCACACCTGTTTGAAGCATTTCCGCTTCACTGATATTCACCA 467  
 322 ACCAGCATCTCTCTTCTTCACTTTATATACGATATGATTAATTAAGATATCT 381  
 468 ATGAGCTGCTTTTCTCATTCACAAACTGATGATGATGAGCTGCTGCTGCTGCTG 527  
 382 TTCGAGAGAACCTTCTGCAAAAGAAAGTTTGTATTTATCTCTTGGCAATTTGG 441  
 528 ATCATTTCACTGATGCTGATTCATTCGATGACCTTCTGATCAATCAACAGAGACC 587  
 442 GTTTTATGATTAACCTTAGAGTTACTACCATCTTCCCTTATTAATCTCTGTTATTA 501

QY 588 AACGATCAGCTGTCTGACCTTACCAAGTTGGATGAATCAATATTAATTAAGTGATC 647  
 DB 502 AATGACACCACTGTATATGATTTTGGAACTTGGAGACCCCAACTCAACCTCATTTAT 561  
 QY 648 AACCTGATTTTGAAGTAACTATCTTGTGCTCCCTTGGGATAGTGAACCTTGGCAT 707  
 DB 562 AGCATGTCTTACACTGTTGGGTTCTTATTTCTCTTTTGTGATGTGTTTCTTTAT 621  
 QY 708 ACCAGAT-----ATCCACACTGTACCCATGAGATGCAACTGACAGCTGCTTAAG 761  
 DB 622 TACAAGATGTGTCTCTCTTAAGACAGAAATGAGAGTGTACTGCTGCTGCTTCCCTT 681  
 QY 762 CAGAAGACAGAGCTTAACCATTTCTGCTACTCTTGCATTTTACGATGTTTAAACC 821  
 DB 682 GAAAAGCTCTCAACTGTGATCATATGAGAGTGAATCTTCTGCTGCTTTTACACCC 741  
 QY 822 TTCAATATCTTGAAGGATCATTTGGATGAATCTGCTGCTTGAATCA-----GTTGT 875  
 DB 742 TATACGTCATGCGGAATGAGAGTGTGCTTACGCTGGGAGTTGAGACAGTATGAG 801  
 QY 876 TCCATGGAATCAGATCCATGAACTTACATGCTTCTAGACCATTAAGCTGCTGTAAC 935  
 DB 802 TGCACTAGGTGCTGATCACTCTTTTATATTTGACACGCTTGGCTTCTGTAAC 861  
 QY 936 ACCTTTGTAACCTGTTACTATATGATGAGTGTGACGACCACTT 979  
 DB 862 AGTGTATCAACCTGCTCTTATTTCTTTTGGAGATCACTT 905

RESULT 14  
 US-10-264-237-1352  
 Sequence 1352, Application US/10264237  
 GENERAL INFORMATION:  
 APPLICANT: Birse et al.  
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 FILE REFERENCE: PA131P1  
 CURRENT APPLICATION NUMBER: US/10/264,237  
 PRIOR FILING DATE: 2002-10-04  
 PRIOR APPLICATION NUMBER: PCT/US01/16450  
 PRIOR FILING DATE: 2001-05-18  
 PRIOR APPLICATION NUMBER: US 60/205,515  
 PRIOR FILING DATE: 2000-05-19  
 NUMBER OF SEQ ID NOS: 2876  
 SOFTWARE: PatentIn Ver. 3.1  
 SEQ ID NO 1352  
 LENGTH: 1436  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-264-237-1352

Query Match 12.1%; Score 131.2; DB 6; Length 1436;  
 Best Local Similarity 49.3%; Pred. No. 5.7e-27;  
 Matches 436; Conservative 0; Mismatches 433; Indels 15; Gaps 3;  
 QY 108 GCTGCTTTTGGAAATTCAGTGAAGAAATCCCACTCAAGATGACCTGCTGTT 167  
 DB 117 GCACCTTGCAAAACTGCTGGCAGCAGAGCTGCTGAAAGTACTACCTTTCATT 176  
 QY 168 ATTATGCGATTATCTCTCTGCGGAAATTCAGGCAATGAGTAGATATTCACCTTAC 227  
 DB 177 TTTATATGGAATGAGTGGTCTGTTGGAGTCTTGGAAATACATTTGTTTACGGGCTAC 236  
 QY 228 ATTTTCAAAATGAGACCTTGGAGAGCAGCAGCATATTATGCTGAACCTGGCTGACA 287  
 DB 237 ATCTTCTCTGGAAGAACTGGAACAGAGATATTTATCTTTTAACTCTGCTCTCT 296  
 QY 288 GATCGCTGATTCAGACAGCTCCCTTCTGATTCATTAATGACAGTGGGAAAC 347  
 DB 297 GACTTACCTTTTCTGTCGACCTCCCATGCTGATTAAGAGTTATGCAATG---AAAC 353  
 QY 348 TGAATCTTTGAGATTTCATGTTGAATTATCCGCTTCACTTCAATTCACCTGAT 407  
 DB 354 TGGATATATGAGAGCGTCTCTGATTAAGCAACGATATGCTTCAATGCAACCTCTAT 413



114 TTGGAAATTCGACTGATGAACAACATCCCACTCAAGATGCACTACCTCCCTGTATTAT 173

```

; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: THORNTON, Michael
; APPLICANT: LU Yan

```

61 TTGGAAATGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCGTATTAT 120  
2y 174 GGCATTAATCTTCTCGTGGGATTTCCAGGCAATGAGATGATTCACATTAATTTT 233  
2b 121 GGCATTAATCTTCTCGTGGGATTTCCAGGCAATGAGATGATTCACATTAATTTT 180  
2y 234 AAATGAGACCTTGGAAGAGAGACCAATCATTAATGCTGAACCTGGCTGACAGATCTG 293  
2b 181 AAATGAGACCTTGGAAGAGAGACCAATCATTAATGCTGAACCTGGCTGACAGATCTG 240  
2y 294 CTGTATCTGACCAAGCTCCCTTCCTGATTTCACTATGACAGTGGGAAACTGATC 353  
2b 241 CTGTATCTGACCAAGCTCCCTTCCTGATTTCACTATGACAGTGGGAAACTGATC 300  
2y 354 TTGGAGATTTCAATGATGTAAGTTATTCGCTTCAAGCTTCCATTTCAACTGTATAGAGC 413  
2b 301 TTGGAGATTTCAATGATGTAAGTTATTCGCTTCAAGCTTCCATTTCAACTGTATAGAGC 360  
2y 414 ATCTCTTCTCCACCTGTTTCAAGATCTTCGGCTACTGATGATCATTCACCCATAGGC 473  
2b 361 ATCTCTTCTCCACCTGTTTCAAGATCTTCGGCTACTGATGATCATTCACCCATAGGC 420  
2y 474 TGCTTTTCCATTCACAAACCTCGATGTCAGTTGATGAGCTGGCTGGTGGATCATTT 533  
2b 421 TGCTTTTCCATTCACAAACCTCGATGTCAGTTGATGAGCTGGCTGGTGGATCATTT 480  
2y 534 TCACTGATGCTGATTCATTCGATGATGATGATGATGATGATGATGATGATGATGATG 593  
2b 481 TCACTGATGCTGATTCATTCGATGATGATGATGATGATGATGATGATGATGATGATG 540  
2y 594 TCAGCTGCTGCTGACCTGACCAAGTGGATGATGATGATGATGATGATGATGATGATG 653  
2b 541 TCAGCTGCTGCTGACCTGACCAAGTGGATGATGATGATGATGATGATGATGATGATG 600  
2y 654 ATTTGATGCTGCACTACTTCTGCTCCCTGGTGGATGATGATGATGATGATGATGATG 713  
2b 601 ATTTGATGCTGCACTACTTCTGCTCCCTGGTGGATGATGATGATGATGATGATGATG 660  
2y 714 ATTTGATGCTGCACTACTTCTGCTCCCTGGTGGATGATGATGATGATGATGATGATG 773  
2b 661 ATTTGATGCTGCACTACTTCTGCTCCCTGGTGGATGATGATGATGATGATGATGATG 720  
2y 774 AGGCTAACCTTCTGCTACTGCTTGGATTTTAACTGATGATGATGATGATGATGATG 833  
2b 721 AGGCTAACCTTCTGCTACTGCTTGGATTTTAACTGATGATGATGATGATGATGATG 780  
2y 834 AGGCTAACCTTCTGCTACTGCTTGGATTTTAACTGATGATGATGATGATGATGATG 893  
2b 781 AGGCTAACCTTCTGCTACTGCTTGGATTTTAACTGATGATGATGATGATGATGATG 840  
2y 894 CATGAGCTTACATCGTTTCTAGACCATAGCTGCTGAAACCTTGGTAACTGTTA 953  
2b 841 CATGAGCTTACATCGTTTCTAGACCATAGCTGCTGAAACCTTGGTAACTGTTA 900  
2y 954 CATATGCTGCTGCTGACGCAAACTTTCAGAGGCTGCTGCTCAACAGTGAAGTGA 1013  
2b 901 CATATGCTGCTGCTGACGCAAACTTTCAGAGGCTGCTGCTCAACAGTGAAGTGA 960  
2y 1014 GTRAGCGGGAACCTTGAAGCAAGCAAAAGATTGTTACTCAAAACAACCTTGA 1067  
2b 961 GTRAGCGGGAACCTTGAAGCAAGCAAAAGATTGTTACTCAAAACAACCTTGA 1014

SEQUENCE 5  
IS-10-321-807-27  
Sequence 27, Application US/10321807  
GENERAL INFORMATION:  
APPLICANT: Chen, Rupong  
APPLICANT: Dang, Hong T.  
APPLICANT: Lowitz, Kevin P.  
TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupled  
FILE REFERENCE: AREN0086

CURRENT APPLICATION NUMBER: US/10/321,807  
PRIOR FILING DATE: 2002-12-16  
PRIOR APPLICATION NUMBER: US/09/714,008  
PRIOR FILING DATE: 2000-11-16  
PRIOR APPLICATION NUMBER: 09/170,496  
PRIOR FILING DATE: 1999-11-17  
PRIOR APPLICATION NUMBER: PCT/US99/23938  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: 60/166,088  
PRIOR FILING DATE: 1999-11-17  
PRIOR APPLICATION NUMBER: 60/166,099  
PRIOR FILING DATE: 1999-11-17  
PRIOR APPLICATION NUMBER: 60/166,369  
PRIOR FILING DATE: 1999-11-17  
PRIOR APPLICATION NUMBER: 60/171,902  
PRIOR FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: 60/171,901  
PRIOR FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: 60/171,900  
PRIOR FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: 60/181,749  
PRIOR FILING DATE: 2000-02-11  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 133  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 27  
LENGTH: 1014  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-321-807-27  
Query Match 93.8%; Score 1014; DB 6; Length 1014;  
Best Local Similarity 100.0%; Pred. No. 5.9e-276;  
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
54 ATGATGAGCCATGACTATTTAGCAAAATGCTTGTGATTTCCCGATTAAGCACTGCT 113  
2b 1 ATGATGAGCCATGACTATTTAGCAAAATGCTTGTGATTTCCCGATTAAGCACTGCT 60  
2y 114 TTGGAAATGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCGTTATTAT 173  
2b 61 TTGGAAATGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCGTTATTAT 120  
2y 174 GGCATTAATCTTCTCGTGGGATTTCCAGGCAATGAGATGATTCACATTAATTTT 233  
2b 121 GGCATTAATCTTCTCGTGGGATTTCCAGGCAATGAGATGATTCACATTAATTTT 180  
2y 234 AAATGAGACCTTGGAAGAGAGACCAATCATTAATGCTGAACCTGGCTGACAGATCTG 293  
2b 181 AAATGAGACCTTGGAAGAGAGACCAATCATTAATGCTGAACCTGGCTGACAGATCTG 240  
2y 294 CTGTATCTGACCAAGCTCCCTTCCTGATTTCACTATGACAGTGGGAAACTGATC 353  
2b 241 CTGTATCTGACCAAGCTCCCTTCCTGATTTCACTATGACAGTGGGAAACTGATC 300  
2y 354 TTGGAGATTTCAATGATGTAAGTTATTCGCTTCAAGCTTCCATTTCAACTGTATAGAGC 413  
2b 301 TTGGAGATTTCAATGATGTAAGTTATTCGCTTCAAGCTTCCATTTCAACTGTATAGAGC 360  
2y 414 ATCTCTTCTCCACCTGTTTCAAGATCTTCGGCTACTGATGATCATTCACCCATAGGC 473  
2b 361 ATCTCTTCTCCACCTGTTTCAAGATCTTCGGCTACTGATGATCATTCACCCATAGGC 420  
2y 474 TGCTTTTCCATTCACAAACCTCGATGTCAGTTGATGAGCTGGCTGGTGGATCATTT 533  
2b 421 TGCTTTTCCATTCACAAACCTCGATGTCAGTTGATGAGCTGGCTGGTGGATCATTT 480  
2y 534 TCACTGATGCTGATTCATTCGATGATGATGATGATGATGATGATGATGATGATGATG 593  
2b 481 TCACTGATGCTGATTCATTCGATGATGATGATGATGATGATGATGATGATGATGATG 540  
2y 594 TCAGCTGCTGCTGACCTGACCAAGTGGATGATGATGATGATGATGATGATGATGATG 653

```

Db 388 GACCTTGGAAGAGAGACCATCATTAATGCTGAAGCTGCGCTGACCAATCTGCTGTATC 447
Qy 301 TGACCAAGCTTCCCTTCTGATTAATCACTAATGCCAGTGGCGAAACTGATCTTTGGAG 360
Db 448 TGACCAAGCTTCCCTTCTGATTAATCACTAATGCCAGTGGCGAAACTGATCTTTGGAG 507
Qy 361 ATTTGATGTAAGTTATCCGCTGAGCTTCCATTTGAACTGTAATGAGCATCTCT 420
Db 508 ATTTGATGTAAGTTATCCGCTGAGCTTCCATTTGAACTGTAATGAGCATCTCT 567
Qy 421 TCCCTACCTGTTTCAGATCTTCCGCTACTGTGTATGATCAATCAACCAATGAGCTGTTT 480
Db 568 TCCCTACCTGTTTCAGATCTTCCGCTACTGTGTATGATCAATCAACCAATGAGCTGTTT 627
Qy 481 CCATTCAAAAATCGATGTGACGTTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
Db 628 CCATTCAAAAATCGATGTGACGTTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 687
Qy 541 TAGCTGTATTCGATGACCTTCTTGTATCAATCAACCAAGAGCAAGCATGAGCTT 600
Db 688 TAGCTGTATTCGATGACCTTCTTGTATCAATCAACCAAGAGCAAGCATGAGCTT 747
Qy 601 GTCTGACCTCACCAAGTTGAGATCAATCAATTAATTAAGTGTAACTGATTTTGA 660
Db 748 GTCTGACCTCACCAAGTTGAGATCAATCAATTAATTAAGTGTAACTGATTTTGA 807
Qy 661 CTGCAACTACTTTCTGCTCTCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Db 808 CTGCAACTACTTTCTGCTCTCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 867
Qy 721 AACCTGTGACCAATGATGATGCAAACTGACAGCTGCTTAAAGCAGAAAGGCTTAA 780
Db 868 AACCTGTGACCAATGATGATGCAAACTGACAGCTGCTTAAAGCAGAAAGGCTTAA 927
Qy 781 CCATTCTGCTACTCTTGTGATTAAGTATGTTTAACTTCCATATCTTGGAGCTCA 840
Db 928 CCATTCTGCTACTCTTGTGATTAAGTATGTTTAACTTCCATATCTTGGAGCTCA 987
Qy 841 TTGCGATGCAATCTGCGCTGCTTCAATCAATGATGATGATGATGATGATGATGATGATG 900
Db 988 TTGCGATGCAATCTGCGCTGCTTCAATCAATGATGATGATGATGATGATGATGATG 1047
Qy 901 CTTAACATGCTTTTAAACCAATTAAGCTGCTGTAACACCTTTGTAACCTGTTACTATATG 960
Db 1048 CTTAACATGCTTTTAAACCAATTAAGCTGCTGTAACACCTTTGTAACCTGTTACTATATG 1107
Qy 961 TGGTGTGACGCAACTTTCAGACAGCTGTCTGTCTCAACAGTGAATGCAAGTAAAGCG 1020
Db 1108 TGGTGTGACGCAACTTTCAGACAGCTGTCTGTCTCAACAGTGAATGCAAGTAAAGCG 1167
Qy 1021 GGAACCTTGAGCAAGCAAAATTAAGTACTCAACCAACCTTGAATATTTCAATTTA 1080
Db 1168 GGAACCTTGAGCAAGCAAAATTAAGTACTCAACCAACCTTGAATATTTCAATTTA 1227
Qy 1081 C 1081
Db 1228 C 1228

```

ESULT 2  
S-10-270-144-3

Sequence 3, Application US/10270144

GENERAL INFORMATION:

APPLICANT: WEI, Ming-Hui et al

TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED

TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR

FILE REFERENCE: CLO00750CON

CURRENT APPLICATION NUMBER: US/10/270,144

PRIOR FILING DATE: 2002-10-15

PRIOR APPLICATION NUMBER: 60/205,196

PRIOR FILING DATE: 2000-05-18

PRIOR FILING DATE: 2000-05-18

```

; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 9905
; TYPE: DNA
; ORGANISM: Human
US-10-270-144-3

Query Match      100.0%; Score 1081; DB 6; Length 9905;
Best Local Similarity 100.0%; Pred. No. 1,6e-294;
Matches 1081; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATATTCGCAAACTGAACTCTCTGTTTCTTTCGAAAGATGAAGAGCAACATGAATG 60
Db 8256 CATATTCGCAAACTGAACTCTCTGTTTCTTTCGAAAGATGAAGAGCAACATGAATG 8315
Qy 61 AGCAGTGAATATTTAGCAAAATGCTTCTGATTTCCCGATTAATGACGCTGTTTGA 120
Db 8316 AGCAGTGAATATTTAGCAAAATGCTTCTGATTTCCCGATTAATGACGCTGTTTGA 8375
Qy 121 ATTGACATGATGAAGAAATCATCCACTCAAGATGACACTGCTCCGTTATTTATGCGATTA 180
Db 8376 ATTGACATGATGAAGAAATCATCCACTCAAGATGACACTGCTCCGTTATTTATGCGATTA 8435
Qy 181 TCTTCTGTGGGATTTTCCAGGCAATGCAAGTATGATATCCATTTCAAAATGA 240
Db 8436 TCTTCTGTGGGATTTTCCAGGCAATGCAAGTATGATATCCATTTCAAAATGA 8495
Qy 241 GACCTTGGAAAGAGAGACCATATTTATGCTGAACCTGGGCTGCAAGATCTGCTATATC 300
Db 8496 GACCTTGGAAAGAGAGACCATATTTATGCTGAACCTGGGCTGCAAGATCTGCTATATC 8555
Qy 301 TGACCAAGCTTCCCTTCTGATTAATGCAATGAGCGGAAACTGATCTTTGGAG 360
Db 8556 TGACCAAGCTTCCCTTCTGATTAATGCAATGAGCGGAAACTGATCTTTGGAG 8615
Qy 361 ATTTGATGTAAGTTATCCGCTTCACTTCAATTTCAACCTGTATAGAGCATCTCT 420
Db 8616 ATTTGATGTAAGTTATCCGCTTCACTTCAATTTCAACCTGTATAGAGCATCTCT 8675
Qy 421 TCCCTACCTGTTTCAGATCTTCCGCTACTGTGTATGATCAATCAACCAATGAGCTGTTT 480
Db 8676 TCCCTACCTGTTTCAGATCTTCCGCTACTGTGTATGATCAATCAACCAATGAGCTGTTT 8735
Qy 481 CCATTCAAAAATCGATGATGCAAGTGTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
Db 8736 CCATTCAAAAATCGATGATGCAAGTGTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8795
Qy 541 TAGCTGTATTCGATGACCTTCTTGTATCAATCAACCAAGAGCAAGATCAAGCTT 600
Db 8796 TAGCTGTATTCGATGACCTTCTTGTATCAATCAACCAAGAGCAAGATCAAGCTT 8855
Qy 601 GTCTGACCTGACCAAGTTGAGATGAATCAATACTATTAAGTGTACCAACCTGATTTTGA 660
Db 8856 GTCTGACCTGACCAAGTTGAGATGAATCAATACTATTAAGTGTACCAACCTGATTTTGA 8915
Qy 661 CTGCAACTACTTTCTGCTCTCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Db 8916 CTGCAACTACTTTCTGCTCTCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8975
Qy 721 ACACTGTGACCCATGAGATGCAAAATGACAGCTGCTTAAAGCAAGAGCTTAA 780
Db 8976 ACACTGTGACCCATGAGATGCAAAATGACAGCTGCTTAAAGCAAGAGCTTAA 9035
Qy 781 CCATTCTGCTACTCTTGTGATTAAGTATGTTTAACTTCCATATCTTGAAGGCTCA 840
Db 9036 CCATTCTGCTACTCTTGTGATTAAGTATGTTTAACTTCCATATCTTGAAGGCTCA 9095
Qy 841 TTGGAATGCAATCTGCGCTGCTTCAATCAAGTGTTCATTTGAATCAATCAATCAATG 900
Db 9096 TTGGAATGCAATCTGCGCTGCTTCAATCAAGTGTTCATTTGAATCAATCAATCAATG 9155
Qy 901 CTTAACATGCTTTTAAACCAATTAAGCTGCTGTAACACCTTTGTAACCTGTTACTATATG 960

```



TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR  
 TITLE OF INVENTION: PROTEINS, AND USES THEREOF  
 FILE REFERENCE: CL000563  
 CURRENT APPLICATION NUMBER: US/60/205,423  
 CURRENT FILING DATE: 2000-05-19  
 NUMBER OF SEQ ID NOS: 494  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 235  
 LENGTH: 8161  
 TYPE: DNA  
 ORGANISM: HUMAN  
 US-60-205-423-235

Query Match 98.8%; Score 1068.4; DB 64; Length 8161;  
 Best Local Similarity 99.8%; Pred. No. 1.9e-295;  
 Matches 1080; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

2Y 1 CATATTGCCAACTGAAGCTCTCTGTTTCTTGGCAAGATGAAGAGACAACATGATG 60  
 Db 3368 CATATTGCCAACTGAAGCTCTCTGTTTCTTGGCAAGATGAAGAGACAACATGATG 3427  
 2Y 61 AGCCACTAGACTATTTCGCAAAATGCTTCTGATTTCCCGATTATGACGCTGTTGGAA 120  
 Db 3428 AGCCACTAGACTATTTCGCAAAATGCTTCTGATTTCCCGATTATGACGCTGTTGGAA 3487  
 2Y 121 ATTGCACTGATGAAATCATCCACTCAAGATGACCTACCTCCCTGTTATTTATGCAATTA 180  
 Db 3488 ATTGCACTGATGAAATCATCCACTCAAGATGACCTACCTCCCTGTTATTTATGCAATTA 3547  
 2Y 181 TCTTCTCGTGGATTTCCAGGCAATGACAGTATGATATCCACTTACCTTTCAAAATGA 240  
 Db 3548 TCTTCTCGTGGATTTCCAGGCAATGACAGTATGATATCCACTTACCTTTCAAAATGA 3607  
 2Y 241 GACCTTGGAAAGACAGACCATCATTAATGCTGAACCTGCTGCAAGATGCTGATATC 300  
 Db 3608 GACCTTGGAAAGACAGACCATCATTAATGCTGAACCTGCTGCAAGATGCTGATATC 3667  
 2Y 301 TGACCAAGCCCTCCCTTCCATTTACCTATGACCAAGTGGGAAAACCTGATCTTTGGAG 360  
 Db 3668 TGACCAAGCCCTCCCTTCCATTTACCTATGACCAAGTGGGAAAACCTGATCTTTGGAG 3727  
 2Y 361 ATTTCATGATGATTTATCCGCTTCACTTCAACCTGATATGAGCAAGCACTCTCT 420  
 Db 3728 ATTTCATGATGATTTATCCGCTTCACTTCAACCTGATATGAGCAAGCACTCTCT 3787  
 2Y 421 TCTCTACCTGTTTCAAGCATCTTCCGCTACTGATGATCATTCACCCATGAGCTGCTTT 480  
 Db 3788 TCTCTACCTGTTTCAAGCATCTTCCGCTACTGATGATCATTCACCCATGAGCTGCTTT 3847  
 2Y 481 CCATTGCAAAATCGATGATGACGTTGATGCTGCTGCTGCTGCTGATCATTTCACTGG 540  
 Db 3848 CCATTGCAAAATCGATGATGACGTTGATGCTGCTGCTGCTGCTGATCATTTCACTGG 3907  
 2Y 541 TAGCTGTCAATCCGATGACCTTCTGATGATCAATCAACCAAGAGCAAGATGACCT 600  
 Db 3908 TAGCTGTCAATCCGATGACCTTCTGATGATCAATCAACCAAGAGCAAGATGACCT 3967  
 2Y 601 GTCTGACCTCAACAGTTGATGAACTCAATATTAAGTGGTCAACCTGATTTTGA 660  
 Db 3968 GTCTGACCTCAACAGTTGATGAACTCAATATTAAGTGGTCAACCTGATTTTGA 4027  
 2Y 661 CTGCAACTATCTTCTGCTCCCTTGGTGGTATGATGACATTTGCTATACCAAGATTAATCC 720  
 Db 4028 CTGCAACTATCTTCTGCTCCCTTGGTGGTATGATGACATTTGCTATACCAAGATTAATCC 4087  
 2Y 721 ACACCTGACCAATGATGACGAAACGACGCTG-CCTTAAGCAAGAAAGACGAGGCTTA 779  
 Db 4088 ACACCTGACCAATGATGACGAAACGACGCTG-CCTTAAGCAAGAAAGACGAGGCTTA 4147  
 2Y 780 ACCATTGCTACTCTCTGCAATTTAAGTATGTTTATACCTTCCATATCTGAGGCTC 839  
 Db 4148 ACCATTGCTACTCTCTGCAATTTAAGTATGTTTATACCTTCCATATCTGAGGCTC 4207

QY 840 ATTGGATGGAATCTGCGCTGTTTCAATCAAGTTTCTTCAATGAAATCAATCATGAA 899  
 Db 4208 ATTGGATGGAATCTGCGCTGTTTCAATCAAGTTTCTTCAATGAAATCAATCATGAA 4267  
 QY 900 GCTTACATGTTTCTAGACCAATAGCTGCTGGAACACCTTGGTAACTGTTACTATAT 959  
 Db 4268 GCTTACATGTTTCTAGACCAATAGCTGCTGGAACACCTTGGTAACTGTTACTATAT 4327  
 QY 960 GTGTGTGTCAGCGCAACTTTCAAGAGCTGCTGCTCAACAGTGAATGCAAGTAAGC 1019  
 Db 4328 GTGTGTGTCAGCGCAACTTTCAAGAGCTGCTGCTCAACAGTGAATGCAAGTAAGC 4387  
 QY 1020 GGGAACTTTGAGCAAGCAAGAAATTAATTACTCAAAACCTTGAATAATTTCAATT 1079  
 Db 4388 GGGAACTTTGAGCAAGCAAGAAATTAATTACTCAAAACCTTGAATAATTTCAATT 4447  
 QY 1080 AC 1081  
 Db 4448 AC 4449

RESULT 15  
 US-60-205-423-236  
 ; Sequence 236, Application US/60205423  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Beasley, Ellen  
 ; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED  
 ; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR  
 ; FILE REFERENCE: CL000563  
 ; CURRENT APPLICATION NUMBER: US/60/205,423  
 ; CURRENT FILING DATE: 2000-05-19  
 ; NUMBER OF SEQ ID NOS: 494  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 236  
 ; LENGTH: 8161  
 ; TYPE: DNA  
 ; ORGANISM: HUMAN  
 ; US-60-205-423-236

Query Match 98.8%; Score 1068.4; DB 64; Length 8161;  
 Best Local Similarity 99.8%; Pred. No. 1.9e-295;  
 Matches 1080; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 CATATTGCCAACTGAAGCTCTCTGTTTCTTGGCAAGATGAAGAGACAACATGATG 60  
 Db 3368 CATATTGCCAACTGAAGCTCTCTGTTTCTTGGCAAGATGAAGAGACAACATGATG 3427  
 QY 61 AGCCACTAGACTATTTCGCAAAATGCTTCTGATTTCCCGATTATGACGCTGTTGGAA 120  
 Db 3428 AGCCACTAGACTATTTCGCAAAATGCTTCTGATTTCCCGATTATGACGCTGTTGGAA 3487  
 QY 121 ATTGCACTGATGAAATCATCCACTCAAGATGACCTACCTCCCTGTTATTTATGCAATTA 180  
 Db 3488 ATTGCACTGATGAAATCATCCACTCAAGATGACCTACCTCCCTGTTATTTATGCAATTA 3547  
 QY 181 TCTTCTCGTGGATTTCCAGGCAATGACAGTATGATATCCACTTACCTTTCAAAATGA 240  
 Db 3548 TCTTCTCGTGGATTTCCAGGCAATGACAGTATGATATCCACTTACCTTTCAAAATGA 3607  
 QY 241 GACCTTGGAAAGACAGACCATCATTAATGCTGAACCTGCTGCAAGATGCTGATATC 300  
 Db 3608 GACCTTGGAAAGACAGACCATCATTAATGCTGAACCTGCTGCAAGATGCTGATATC 3667  
 QY 301 TGACCAAGCTCCCTTCCATTTACCTATGACCAAGTGGGAAAACCTGATCTTTGGAG 360  
 Db 3668 TGACCAAGCTCCCTTCCATTTACCTATGACCAAGTGGGAAAACCTGATCTTTGGAG 3727  
 QY 361 ATTTCATGATGATTTATCCGCTTCACTTCAACCTGATATGAGCAAGCACTCTCT 420  
 Db 3728 ATTTCATGATGATTTATCCGCTTCACTTCAACCTGATATGAGCAAGCACTCTCT 3787  
 QY 421 TCTCTACCTGTTTCAAGCATCTTCCGCTACTGATGATCATTCACCCATGAGCTGCTTT 480

LENGTH: 43262  
 TYPE: DNA  
 ORGANISM: Human  
 US-60-261-974-40

Query Match 99.9%; Score 1079.4; DB 70; Length 43262;  
 Best Local Similarity 99.9%; Pred. No. 2.9e-298;  
 Matches 1080; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 CATATTGCCAACTGAACTCTCTGTTTCTTGGCAAGTGAAGAGACACATGAATG 60  
 1949 CATATTGCCAACTGAACTCTCTGTTTCTTGGCAAGTGAAGAGACACATGAATG 2008  
 61 AGCCACTAGACTATTGAGAAATGCTTCTGATTTCCCGATTATGACAGCTCTTGGAA 120  
 2009 AGCCACTAGACTATTGAGAAATGCTTCTGATTTCCCGATTATGACAGCTCTTGGAA 2068  
 121 ATTGCACTGATGAAACATCTCCACTCAAGATGACATCTCCCTGTTATTTATGGCATT 180  
 2069 ATTGCACTGATGAAACATCTCCACTCAAGATGACATCTCCCTGTTATTTATGGCATT 2128  
 181 TCTTCTCGGGGATTTCCAGGCAATGACATGATATCCACTTAATTTCAAAATGA 240  
 2129 TCTTCTCGGGGATTTCCAGGCAATGACATGATATCCACTTAATTTCAAAATGA 2188  
 241 GACCTTGAAGAGACAGACCATCATTAATGCTGAACCTGGCTGACAGATCTGCTATC 300  
 2189 GACCTTGAAGAGACAGACCATCATTAATGCTGAACCTGGCTGACAGATCTGCTATC 2248  
 301 TGACCGCTCTCCCTCTCTGATTCATCTATGCGACGTGGGAAATCGATCTTTGGAG 360  
 2249 TGACCGCTCTCCCTCTCTGATTCATCTATGCGACGTGGGAAATCGATCTTTGGAG 2308  
 361 ATTTCATGTAAGTTTATCCGCTGAGCTTCACTTCAACCTGTATAGACAGATCTCT 420  
 2309 ATTTCATGTAAGTTTATCCGCTGAGCTTCACTTCAACCTGTATAGACAGATCTCT 2368  
 421 TCCCTCACTGTTTACAGCATCTTCCGCTACTGTGATCATTTCAACCAATAGAGCTGCTT 480  
 2369 TCCCTCACTGTTTACAGCATCTTCCGCTACTGTGATCATTTCAACCAATAGAGCTGCTT 2428  
 481 CCATTTCACAAAATCGATGTGACAGTTGTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 540  
 2429 CCATTTCACAAAATCGATGTGACAGTTGTGTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 2488  
 541 TAGCTGTCAATCCGATGACCTTTTATCATCATCAACCAAGAGCAATGATCAGCT 600  
 2489 TAGCTGTCAATCCGATGACCTTTTATCATCATCAACCAAGAGCAATGATCAGCT 2548  
 601 GTCGTGACCTCAACAGTTGGAGTGAATCAATCTATTAAGTGTATACCTGATTTTGA 660  
 2549 GTCGTGACCTCAACAGTTGGAGTGAATCAATCTATTAAGTGTATACCTGATTTTGA 2608  
 661 CTGCAACTATCTTCTGCTCCCTCTGATGATGACATTTGCTATTAACCAAGATTTATCC 720  
 2609 CTGCAACTATCTTCTGCTCCCTCTGATGATGACATTTGCTATTAACCAAGATTTATCC 2668  
 721 ACACGTGACCAATGATGACAAATGACAGCTGCTTAAAGCAAAAGCAAGAGGTTA 780  
 2669 ACACGTGACCAATGATGACAAATGACAGCTGCTTAAAGCAAAAGCAAGAGGTTA 2728  
 781 CCATTCTGCTACTCTTGTGATTTTATAGTATGTTTATACCTTCCATATTTTGAAGGTTCA 840  
 2729 CCATTCTGCTACTCTTGTGATTTTATAGTATGTTTATACCTTCCATATTTTGAAGGTTCA 2788  
 841 TTCCGATGAAATCTGCGCTGCTTTCATGAGTTTTCATTTGAGATTCAGATCATGAAG 900  
 2789 TTCCGATGAAATCTGCGCTGCTTTCATGAGTTTTCATTTGAGATTCAGATCATGAAG 2848  
 901 CTTCATGCTTTCTAGACATTAAGTGTCTGAAACACTTTGGTAACTGTTTACTATATG 960  
 2849 CTTCATGCTTTCTAGACATTAAGTGTCTGAAACACTTTGGTAACTGTTTACTATATG 2908

Qy 961 TGTGTGTCAGGCAACTTTTCAGAGGCTGTCTCTCAACAGTGAATGCAAAAGTAAACG 1020  
 Db 2909 TGTGTGTCAGGCAACTTTTCAGAGGCTGTCTCTCAACAGTGAATGCAAAAGTAAACG 2968  
 Qy 1021 GGAACCTTGAGCAAGCAAGAAATTTAGTATCTCAACCAACCTTGAATATTTCAATTA 1080  
 Db 2969 GGAACCTTGAGCAAGCAAGAAATTTAGTATCTCAACCAACCTTGAATATTTCAATTA 3028  
 Qy 1081 C 1081  
 Db 3029 C 3029

## RESULT 12

US-60-205-423-233  
 ; Sequence 233, Application US/60205423  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Beasley, Ellen  
 ; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED  
 ; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR  
 ; TITLE OF INVENTION: PROTEINS, AND USES THEREOF  
 ; FILE REFERENCE: CL000563  
 ; CURRENT APPLICATION NUMBER: US/60/205,423  
 ; CURRENT FILING DATE: 2000-05-19  
 ; NUMBER OF SEQ ID NOS: 494  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 233  
 ; LENGTH: 8161  
 ; TYPE: DNA  
 ; ORGANISM: HUMAN  
 ; US-60-205-423-233

Query Match 98.8%; Score 1068.4; DB 64; Length 8161;  
 Best Local Similarity 99.8%; Pred. No. 1.9e-295;  
 Matches 1080; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 CATATTGCCAACTGAACTCTCTGTTTCTTGGCAAGTGAAGAGACACATGAATG 60  
 Db 3368 CATATTGCCAACTGAACTCTCTGTTTCTTGGCAAGTGAAGAGACACATGAATG 3427  
 Qy 61 AGCCACTAGACTATTGAGAAATGCTTCTGATTTCCCGATTATGACAGCTCTTGGAA 120  
 Db 3428 AGCCACTAGACTATTGAGAAATGCTTCTGATTTCCCGATTATGACAGCTCTTGGAA 3487  
 Qy 121 ATTGCACTGATGAAACATCTCCACTCAAGATGACATCTCCCTGTTATTTATGGCATT 180  
 Db 3488 ATTGCACTGATGAAACATCTCCACTCAAGATGACATCTCCCTGTTATTTATGGCATT 3547  
 Qy 181 TCTTCTCGGGGATTTCCAGGCAATGACATGATATCCACTTAATTTCAAAATGA 240  
 Db 3548 TCTTCTCGGGGATTTCCAGGCAATGACATGATATCCACTTAATTTCAAAATGA 3607  
 Qy 241 GACCTTGAAGAGACAGACCATCATTAATGCTGAACCTGGCTGACAGATCTGCTATC 300  
 Db 3608 GACCTTGAAGAGACAGACCATCATTAATGCTGAACCTGGCTGACAGATCTGCTATC 3667  
 Qy 301 TGACCAAGCTCTCCCTCTCTGATTCATCTATGCGACGTGGGAAATCGATCTTTGGAG 360  
 Db 3668 TGACCAAGCTCTCCCTCTCTGATTCATCTATGCGACGTGGGAAATCGATCTTTGGAG 3727  
 Qy 361 ATTTCATGTAAGTTTATCCGCTGAGCTTCCATTTCAACCTGTATAGAGAGATCTCT 420  
 Db 3728 ATTTCATGTAAGTTTATCCGCTGAGCTTCCATTTCAACCTGTATAGAGAGATCTCT 3787  
 Qy 421 TCCCTCACTGTTTACAGCATCTTCCGCTACTGTGATCATTTCAACCAATAGAGCTGCTT 480  
 Db 3788 TCCCTCACTGTTTACAGCATCTTCCGCTACTGTGATCATTTCAACCAATAGAGCTGCTT 3847  
 Qy 481 CCATTTCACAAAATCGATGTGACAGTTGTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 540  
 Db 3848 CCATTTCACAAAATCGATGTGACAGTTGTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 3907  
 Qy 541 TAGCTGTCAATCCGATGACCTTTTATCATCATCAACCAAGAGCAATGATCAGCT 600



```

FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17
; OTHER INFORMATION: n = A,T,C or G
US-09-785-276A-29927

Query Match      99.9%; Score 1079.4; DB 30; Length 1729;
Beet Local Similarity 99.9%; Pred. No. 6.2e-299;
Matches 1080; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  CATATGGCCAAACGAACTCTCTGTGTTTCTTTGCAAGATGAAAGGACCAACGATGAATG 60
Db      241 CATATGGCCAAACGAACTCTCTGTGTTTCTTTGCAAGATGAAAGGACCAACGATGAATG 300

QY      61  AGCCACTGACCTATTATAGCAATGCTTCTGATTTCCCGATTATGACAGTGGTTTGAA 120
Db      301 AGCCACTGACCTATTATAGCAATGCTTCTGATTTCCCGATTATGACAGTGGTTTGAA 360

QY      121 ATTGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTATTTATGACATTA 180
Db      361 ATTGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTATTTATGACATTA 420

QY      181 TCTTCTCTGTGGGATTTCCAGGCAATGCAAGTAGTAGATATCCATTTACATTTTCAAAATGA 240
Db      421 TCTTCTCTGTGGGATTTCCAGGCAATGCAAGTAGTAGATATCCATTTTCAAAATGA 480

QY      241 GACCTTGGAAAGCAGCACCATCATATATAGCTGAACCTGGCTGCACAGATCTGCTGATC 300
Db      481 GACCTTGGAAAGCAGCACCATCATATATAGCTGAACCTGGCTGCACAGATCTGCTGATC 540

QY      301 TGACAGAGCTCCCTCCCTCCGATGATCACTATGACAGTAGGGGAAAACGTGATCTTTGGAG 360
Db      541 TGACAGAGCTCCCTCCCTCCGATGATCACTATGACAGTAGGGGAAAACGTGATCTTTGGAG 600

QY      361 ATTTCATATGTATGATTATTCGCTTACGCTTCCATTTCAACCTGTATAGACATCTCT 420
Db      601 ATTTCATATGTATGATTATTCGCTTACGCTTCCATTTCAACCTGTATAGACATCTCT 660

QY      421 TCTTCACCTGTTTTCAGACATCTTCGCTACTGTGTGATCATTTACCCCAATGAGCTGCTTTT 480

```

[illegible]

```

APPLICANT: White, David
TITLE OF INVENTION: Novel Seven-Transmembrane
FILE REFERENCE: 5800-67
CURRENT APPLICATION NUMBER: US/09/475,790
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1729
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (294)...(1307)
US-09-475-790-2

```

Query Match 99.9%; Score 1079.4; DB 18; Length 1729;  
Best Local Similarity 99.9%; Pred. No. 6.2e-299;  
Matches 1080; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy 1 CATATGGCAAGTGAAGTCTCTGTTTCTTGGCAAGATGAAAGACACCATGATG 60
Db 241 CATATGGCAAGTGAAGTCTCTGTTTCTTGGCAAGATGAAAGACACCATGATG 300
Qy 61 AGCCACTGAGCTATTAGCAATGCTTGATTTCCCGATTATGAGCTGTTTGA 120
Db 301 AGCCACTGAGCTATTAGCAATGCTTGATTTCCCGATTATGAGCTGTTTGA 360
Qy 121 ATTGCACTGATGAAAAACATCCCACTCAAGATGACATACCTCCCTGTTATTTATGACATTA 180
Db 361 ATTGCACTGATGAAAAACATCCCACTCAAGATGACATACCTCCCTGTTATTTATGACATTA 420
Qy 181 TCTTCCTCTGTGGGATTTTCCAGGCAATGCAATGATGATTCACCTTATTTCAAAATGA 240
Db 421 TCTTCCTCTGTGGGATTTTCCAGGCAATGCAATGATGATTCACCTTATTTCAAAATGA 480
Qy 241 GACCTTGGAGAGAGAGACACATCATTTATGCTGAGCTGGCCGCGACAGATTCGCTGATC 300
Db 481 GACCTTGGAGAGAGAGACACATCATTTATGCTGAGCTGGCCGCGACAGATTCGCTGATC 540
Qy 301 TGACCAAGCTCCCTCTCTGATTCATCTACTATGCGAGTGGCAAAATGATCTTTGGAG 360
Db 541 TGACCAAGCTCCCTCTCTGATTCATCTACTATGCGAGTGGCAAAATGATCTTTGGAG 600
Qy 361 ATTTCATGATGATGATTTATCGGCTTCACTTCCATTTCAACCTGTATAGCAATCTCT 420
Db 601 ATTTCATGATGATGATTTATCGGCTTCACTTCCATTTCAACCTGTATAGCAATCTCT 660
Qy 421 TCCGCACTGTTTGAAGCATCTTCCGCTACTGTGATCATTTCAACCTGTATAGCAATCTCT 480
Db 661 TCCGCACTGTTTGAAGCATCTTCCGCTACTGTGATCATTTCAACCTGTATAGCAATCTCT 720
Qy 481 CCATTGCAAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Db 721 CCATTGCAAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Qy 541 TAGCTGATTTCCGATGATCTTCTTGTATCATCATCAACCAAGCAAGCATGAGCT 600
Db 781 TAGCTGATTTCCGATGATCTTCTTGTATCATCATCAACCAAGCAAGCATGAGCT 840
Qy 601 GTCTGCACTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db 841 GTCTGCACTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
Qy 661 CTGCAATCTACTTCTGCTCCCTCTTGTGATGATGATGATGATGATGATGATGATGATGAT 720
Db 901 CTGCAATCTACTTCTGCTCCCTCTTGTGATGATGATGATGATGATGATGATGATGATGAT 960
Qy 721 ACACTGACCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 780
Db 961 ACACTGACCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1020

```

```

Qy 781 CCATTCTGCTACTCCCTGATTTTAAGTATGTTTAAACCTTCATATCTTGAAGGTCA 840
Db 1021 CCATTCTGCTACTCCCTGATTTTAAGTATGTTTAAACCTTCATATCTTGAAGGTCA 1080
Qy 841 TTGGATGCAATCTGCGCTCTTCAATCATGTTTTCATATGAGATGATCATGAG 900
Db 1081 TTGGATGCAATCTGCGCTCTTCAATCATGTTTTCATATGAGATGATCATGAG 1140
Qy 901 CTTCATGCTTTCTGACCATTAAGTGTGCTGTGACACCTTTGGTAACTGTATATATG 960
Db 1141 CTTCATGCTTTCTGACCATTAAGTGTGCTGTGACACCTTTGGTAACTGTATATATG 1200
Qy 961 TGGTGTGAGGAGCACTTTCAGCAGGCTGTGCTCAACAGTGAAGTGAAGTGAAGTGAAGTGA 1020
Db 1201 TGGTGTGAGGAGCACTTTCAGCAGGCTGTGCTCAACAGTGAAGTGAAGTGAAGTGAAGTGA 1260
Qy 1021 GGAACCTTGAGCAAGCAAGAAATTTAGTACTCAACACCTTGAATATTTCAATTA 1080
Db 1261 GGAACCTTGAGCAAGCAAGAAATTTAGTACTCAACACCTTGAATATTTCAATTA 1320
Qy 1081 C 1081
Db 1321 C 1321

```

```

RESULT 7
US-09-785-276A-24015
Sequence 24015, Application US/09785276A
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
IDENTIFICATION, IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
FILE REFERENCE: MRI-0078
CURRENT APPLICATION NUMBER: US/09/785,276A
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24015
LENGTH: 1729
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17
OTHER INFORMATION: n = A,T,C or G
US-09-785-276A-24015

```

```

Query Match 99.9%; Score 1079.4; DB 30; Length 1729;
Best Local Similarity 99.9%; Pred. No. 6.2e-299;
Matches 1080; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CATATGGCAAGTGAAGTCTCTGTTTCTTGGCAAGATGAAAGACACCATGATG 60
Db 241 CATATGGCAAGTGAAGTCTCTGTTTCTTGGCAAGATGAAAGACACCATGATG 300
Qy 61 AGCCACTGAGCTATTAGCAATGCTTGATTTCCCGATTATGAGCTGTTTGA 120
Db 301 AGCCACTGAGCTATTAGCAATGCTTGATTTCCCGATTATGAGCTGTTTGA 360

```

Db 421 TCCTCACTGTTTACGATCTTCGCTACTGTGTGATCATTCACCCATGAGCTCTTT 480  
Qy 481 CCATTGACAAAATCCGATGTGCAAGTTGAGCTGTGTGTGTGTGATCATTTTCACTGG 540  
Db 481 CCATTGACAAAATCCGATGTGCAAGTTGAGCTGTGTGTGTGTGATCATTTTCACTGG 540  
Qy 541 TAGCTGTGATTCGGATGACCTTCTGTGATCATCAACCAAGAGCCAAAGATCAAGCTT 600  
Db 541 TAGCTGTGATTCGGATGACCTTCTGTGATCATCAACCAAGAGCCAAAGATCAAGCTT 600  
Qy 601 GTCTGACCTCACAGTTCGGATGATCACTATATTAAGTGTGACCACTGATTTTGA 660  
Db 601 GTCTGACCTCACAGTTCGGATGATCACTATATTAAGTGTGACCACTGATTTTGA 660  
Qy 661 CTGCAACTACTTCTTGTGCTTCCCTTGTGTGATGTGACACTTGTCTATACAGATTATCC 720  
Db 661 CTGCAACTACTTCTTGTGCTTCCCTTGTGTGATGTGACACTTGTCTATACAGATTATCC 720  
Qy 721 ACACCTGACCCGATGACCTGCAAACTGACGTGCTTAAGCAGAAAGCAGAGGCTTA 780  
Db 721 ACACCTGACCCGATGACCTGCAAACTGACGTGCTTAAGCAGAAAGCAGAGGCTTA 780  
Qy 781 CCATTCTGACTACTCTTGTGACATTTTAACTGATGTTTAACTTCAATCTTGAAGGCTCA 840  
Db 781 CCATTCTGACTACTCTTGTGACATTTTAACTGATGTTTAACTTCAATCTTGAAGGCTCA 840  
Qy 841 TTGCGATGCAATCTCGCTGCTTCAATCACTGATGTTTCAATGAGATCAATCCATGAG 900  
Db 841 TTGCGATGCAATCTCGCTGCTTCAATCACTGATGTTTCAATGAGATCAATCCATGAG 900  
Qy 901 CTTAACATGCTTTTCTAGACCATTAAGTGTGTGTGACACCTTGTGTGATCTGTATATG 960  
Db 901 CTTAACATGCTTTTCTAGACCATTAAGTGTGTGTGACACCTTGTGTGATCTGTATATG 960  
Qy 961 TGGTGTGACGACCACTTTCAGCAGGCTGTCTCTCAACAGTGTGACCAAGTAAAGCG 1020  
Db 961 TGGTGTGACGACCACTTTCAGCAGGCTGTCTCTCAACAGTGTGACCAAGTAAAGCG 1020  
Qy 1021 GGAACCTTGAGCAAGCAAAATAATGATTAAGTCAACCAACCTTGAATAATTTCAATTA 1080  
Db 1021 GGAACCTTGAGCAAGCAAAATAATGATTAAGTCAACCAACCTTGAATAATTTCAATTA 1080  
Qy 1081 C 1081  
Db 1081 C 1081

RESULT 4  
JS-09-634-656-3  
; Sequence 3, Application US/09634656  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Ming-Hui et al  
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED  
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR  
; FILE REFERENCES: C1000750  
; CURRENT APPLICATION NUMBER: US/09/634,656  
; CURRENT FILING DATE: 2000-08-08  
; PRIOR APPLICATION NUMBER: 60/205,196  
; PRIOR FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 9905  
; TYPE: DNA  
; ORGANISM: Human  
JS-09-634-656-3

Query Match 100.0%; Score 1081; DB 24; Length 9905;  
Best Local Similarity 100.0%; Pred. No. 4,9e-299;  
Matches 1081; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CANATTGCCAAGCAAGCACTCTTGTGTTTCTTGTGCAAGATGAAGAGCAACCATGAATG 60

Db 8256 CATATTGCCAAGCAAGCACTCTTGTGTTTCTTGTGCAAGATGAAGAGCAACCATGAATG 8315  
Qy 61 AGCCATGACATATTAGCAAAATGCTTCTGATTTCCCGATTATGACAGCTCTTTGGAA 120  
Db 8316 AGCCATGACATATTAGCAAAATGCTTCTGATTTCCCGATTATGACAGCTCTTTGGAA 8375  
Qy 121 ATTGCACTGATGAAGAACATCCCACTCAAGATGACATACCTCCCTGTTATTTATGGCATTA 180  
Db 8376 ATTGCACTGATGAAGAACATCCCACTCAAGATGACATACCTCCCTGTTATTTATGGCATTA 8435  
Qy 181 TCTTCCTGTGGGATTTCCAGGGCAATGCAAGTATATCCACTTACATTTTCAAAATGA 240  
Db 8436 TCTTCCTGTGGGATTTCCAGGGCAATGCAAGTATATCCACTTACATTTTCAAAATGA 8495  
Qy 241 GACCTTGAAGAGCAGACCATCATTAATGCTGAACCTGACCTGACAGATGTGCTGATC 300  
Db 8496 GACCTTGAAGAGCAGACCATCATTAATGCTGAACCTGACCTGACAGATGTGCTGATC 8555  
Qy 301 TGACCAAGCTTCCCTTCTGATTTCACTATATGCAAGTGTGCAAACTGATCTTTGGAG 360  
Db 8556 TGACCAAGCTTCCCTTCTGATTTCACTATATGCAAGTGTGCAAACTGATCTTTGGAG 8615  
Qy 361 ATTTCATGTGAAATTTATGCGCTTCAAGCTTCCATTTCAACCTGTATAGCATCTCT 420  
Db 8616 ATTTCATGTGAAATTTATGCGCTTCAAGCTTCCATTTCAACCTGTATAGCATCTCT 8675  
Qy 421 TCCTCACTGTTTACGATCTTCCGCTACTGTGTGATCATTCACCAATGAGCTCTTT 480  
Db 8676 TCCTCACTGTTTACGATCTTCCGCTACTGTGTGATCATTCACCAATGAGCTCTTT 8735  
Qy 481 CCATTGACAAAATCCGATGTGCAAGTTGAGCTGTGTGTGTGTGATCATTTTCACTGG 540  
Db 8736 CCATTGACAAAATCCGATGTGCAAGTTGAGCTGTGTGTGTGTGATCATTTTCACTGG 8795  
Qy 541 TAGCTGTGATTCGGATGACCTTCTGTGATCAATCAACCAAGAGCCAAAGATCAAGCTT 600  
Db 8796 TAGCTGTGATTCGGATGACCTTCTGTGATCAATCAACCAAGAGCCAAAGATCAAGCTT 8855  
Qy 601 GTCTGACCTCACAGTTCGGATGATCACTATATTAAGTGTGACCACTGATTTTGA 660  
Db 8856 GTCTGACCTCACAGTTCGGATGATCACTATATTAAGTGTGACCACTGATTTTGA 8915  
Qy 661 CTGCAACTACTTCTTGTGCTTCCCTTGTGTGATGTGACACTTGTATACAGATTATCC 720  
Db 8916 CTGCAACTACTTCTTGTGCTTCCCTTGTGTGATGTGACACTTGTATACAGATTATCC 8975  
Qy 721 ACACCTGACCCGATGACCTGCAAACTGACGTGCTTAAGCAGAAAGCAGAGGCTTA 780  
Db 8976 ACACCTGACCCGATGACCTGCAAACTGACGTGCTTAAGCAGAAAGCAGAGGCTTA 9035  
Qy 781 CCATTCTGACTACTCTTGTGACATTTTAACTGATGTTTAACTTCAATCTTGAAGGCTCA 840  
Db 9036 CCATTCTGACTACTCTTGTGACATTTTAACTGATGTTTAACTTCAATCTTGAAGGCTCA 9095  
Qy 841 TTGCGATGCAATCTCGCTGCTTCAATCACTGATGTTTCAATGAGATCAATCCATGAG 900  
Db 9096 TTGCGATGCAATCTCGCTGCTTCAATCACTGATGTTTCAATGAGATCAATCCATGAG 9155  
Qy 901 CTTAACATGCTTTCTAGACCATTAAGTGTGTGTGACACCTTGTGTGATCTGTATATG 960  
Db 9156 CTTAACATGCTTTCTAGACCATTAAGTGTGTGTGACACCTTGTGTGATCTGTATATG 9215  
Qy 961 TGGTGTGACGACCACTTTCAGCAGGCTGTCTCTCAACAGTGTGACCAAGTAAAGCG 1020  
Db 9216 TGGTGTGACGACCACTTTCAGCAGGCTGTCTCTCAACAGTGTGACCAAGTAAAGCG 9275  
Qy 1021 GGAACCTTGAGCAAGCAAAATAATGATTAAGTCAACCAACCTTGAATAATTTCAATTA 1080  
Db 9276 GGAACCTTGAGCAAGCAAAATAATGATTAAGTCAACCAACCTTGAATAATTTCAATTA 9335  
Qy 1081 C 1081

```

22 1068.4 98.8 11303 64 US-60-200-364-46 Sequence 46, Appl
23 1068.4 98.8 11303 64 US-60-200-364-47 Sequence 47, Appl
24 1068.4 98.8 11303 64 US-60-200-364-48 Sequence 48, Appl
25 1068.4 98.8 11303 64 US-60-200-364-49 Sequence 49, Appl
26 1068.4 98.8 11303 64 US-60-200-364-50 Sequence 50, Appl
27 1068.4 98.8 11303 64 US-60-200-364-51 Sequence 51, Appl
28 1068.4 98.8 11303 64 US-60-200-364-52 Sequence 52, Appl
29 1068.4 98.8 11303 64 US-60-200-364-53 Sequence 53, Appl
30 1068.4 98.8 11303 64 US-60-200-364-54 Sequence 54, Appl
31 1058 97.9 1068 75 US-60-311-340-1 Sequence 1, Appl
32 1014 93.8 1014 24 US-09-634-656-1 Sequence 1, Appl
33 1014 93.8 1014 28 US-09-714-008A-27 Sequence 27, Appl
34 1014 93.8 1014 33 US-09-885-453-2 Sequence 2, Appl
35 1014 93.8 1014 35 US-09-943-798-3 Sequence 3, Appl
36 1014 93.8 1014 37 US-09-955-543-27 Sequence 27, Appl
37 1014 93.8 1014 39 US-10-079-384-13 Sequence 13, Appl
38 1014 93.8 1014 39 US-10-096-511-27 Sequence 27, Appl
39 1013.4 93.7 1015 65 US-60-212-655-973 Sequence 973, Appl
40 1012.4 93.7 1014 22 US-09-569-137-1 Sequence 22, Appl
41 1012.4 93.7 1014 37 US-09-988-922-33 Sequence 33, Appl
42 1012.4 93.7 1014 38 US-10-023-775B-1 Sequence 1, Appl
43 1012.4 93.7 1014 40 US-10-125-748-33 Sequence 33, Appl
44 1012.4 93.7 1014 64 US-60-207-556-2 Sequence 2, Appl
45 1012.4 93.7 1015 66 US-60-229-515-1722 Sequence 1722, Ap

```

## ALIGNMENTS

## RESULT 1

```

US-10-010-568-1
: Sequence 1, Application US/10010568
: GENERAL INFORMATION:
: APPLICANT: Bristol-Myers Squibb Company
: TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBM23, EXPRESSED HI
: TITLE OF INVENTION: KIDNEY
: FILE REFERENCE: D0077 NP
: CURRENT APPLICATION NUMBER: US/10/010,568
: CURRENT FILING DATE: 2001-12-07
: PRIOR APPLICATION NUMBER: US 60/251,926
: PRIOR FILING DATE: 2000-12-07
: PRIOR APPLICATION NUMBER: US 60/269,795
: PRIOR FILING DATE: 2001-02-14
: NUMBER OF SEQ ID NOS: 55
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 1
: LENGTH: 1081
: TYPE: DNA
: ORGANISM: homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (54)..(1064)
US-10-010-568-1

```

Query Match 100.0%; Score 1081; DB 38; Length 1081;

Best Local Similarity 100.0%; Pred. No. 1.7e-293; Matches 1081; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 CATATTGCCAACTGAACTCTCTGTTGTTTCTTGCAGATGAAAGAGACAACATGAATG 60
Db 1 CATATTGCCAACTGAACTCTCTGTTTCTTGCAGATGAAAGAGACAACATGAATG 60
QY 61 AGCAGTGAAGTATTTAGCAATGCTTGTGATTTCCCGATTAGCAGCTGTTTGAA 120
Db 61 AGCAGTGAAGTATTTAGCAATGCTTGTGATTTCCCGATTAGCAGCTGTTTGAA 120
QY 121 ATTGACATGATGAAGATCCCACTCAAGATGACCTACCTCCGTTTATTTATGACATTA 180
Db 121 ATTGACATGATGAAGATCCCACTCAAGATGACCTACCTCCGTTTATTTATGACATTA 180
QY 181 TCTTCTCTGTTGGATTTCCAGGCAATGAGATGATATTCACACTTATTTCAAAAATGA 240
Db 181 TCTTCTCTGTTGGATTTCCAGGCAATGAGATGATATTCACACTTATTTCAAAAATGA 240

```

```

QY 241 GACCTTGAAGAGACAGACCATCATATATGCTGAACCTGGCTGACAGATCTGCTATC 300
Db 241 GACCTTGAAGAGACAGACCATCATATATGCTGAACCTGGCTGACAGATCTGCTATC 300
QY 301 TGACAGAGCTCCCTCTCTGATTTACTATGCTATGCTGAGTGGGAAATCTGATCTTTGAG 360
Db 301 TGACAGAGCTCCCTCTCTGATTTACTATGCTATGCTGAGTGGGAAATCTGATCTTTGAG 360
QY 361 ATTTCATGATGATATTTATGCTGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 420
Db 361 ATTTCATGATGATATTTATGCTGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 420
QY 421 TCTTCACCTGTTTCAAGATCTTCCGCTACTGCTGATGATCACTTCACTTCACTTCACTTCACT 480
Db 421 TCTTCACCTGTTTCAAGATCTTCCGCTACTGCTGATGATCACTTCACTTCACTTCACTTCACT 480
QY 481 CCATTGCAAAATCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Db 481 CCATTGCAAAATCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 541 TAGCTGATTTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Db 541 TAGCTGATTTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 601 GTCTGACCTGACAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db 601 GTCTGACCTGACAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 661 CTGCAACTATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
Db 661 CTGCAACTATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
QY 721 ACATCTGACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Db 721 ACATCTGACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY 781 CCATTGCTACTCTCTGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
Db 781 CCATTGCTACTCTCTGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 841 TTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
Db 841 TTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 901 CTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Db 901 CTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
QY 961 TGGTGGTACGACAACTTTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Db 961 TGGTGGTACGACAACTTTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1021 GGAACCTTGAAGCAAAATTTAGTACTCAACCACTTGAATATTTATTTA 1080
Db 1021 GGAACCTTGAAGCAAAATTTAGTACTCAACCACTTGAATATTTATTTA 1080
QY 1081 C 1081
Db 1081 C 1081

```

## RESULT 2

```

US-60-251-926-1
: Sequence 1, Application US/60251926
: GENERAL INFORMATION:
: APPLICANT: Bristol-Myers Squibb Company
: TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBM23, EXPRESSED I
: TITLE OF INVENTION: KIDNEY
: FILE REFERENCE: D0077 PSP
: CURRENT APPLICATION NUMBER: US/60/251,926
: CURRENT FILING DATE: 2000-12-07
: NUMBER OF SEQ ID NOS: 35

```

CURRENT APPLICATION NUMBER: US/09/962,832  
 CURRENT FILING DATE: 2001-09-25  
 PRIOR APPLICATION NUMBER: US/60/235,077  
 PRIOR FILING DATE: 2000-09-25  
 PRIOR APPLICATION NUMBER: US/60/235,280  
 PRIOR FILING DATE: 2000-09-25  
 NUMBER OF SEQ ID NOS: 259  
 SOFTWARE: PatentIn version 3.0

SEQ ID NO 218  
 LENGTH: 2051  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-962-832-218

Query Match  
 Best Local Similarity 7.7%; Score 82.8; DB 10; Length 2051;  
 Matches 186; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

2y 183 TTCTCGTGGGATTTCCAGGCAATGCAATGATGATTCACCTTACATTTTCAAAATGAGA 242  
 Db 172 TTATCTTTGGGCTTGGGCAATGGCTTGCCTGTGGATTTCTGTTCCACCTCAAG 231  
 2y 243 CCTTGAAGAGCAGCACCACATCATATGCTGAACCTGGCTGACAGATCTGCTATCTG 302  
 Db 232 TCCTGGAATCCAGCCGGAATTTCTCTTCAACCTGAGAGTGAAGCTTCTACTGATC 291  
 2y 303 ACCAGCTCCCTCCCTCCGATGATCACTATAGCCAGTGGCAAACTGGATCTTTGAGAT 362  
 Db 292 ATCTGCTGCGCTTGGATGAGTACTATATGCGGCTTCAAGTGAACCTTTGGGGAC 351  
 2y 363 TTCATGTGATGATTTATCCGCTTCCAGCTTCCATTTCAACCTGTATAGAGCATCCTTTC 422  
 Db 352 ATCCCTTGGCCGCTGCTGCTTCTTATGTTGCCATGAAACCCGAGGAGCATCATCTTC 411  
 2y 423 CTCACCTGTTTACGATCTTCCGCTACTGTGTGATCATTTACCCATGAGCTGCTTTTC 482  
 Db 412 CTCACGCTGTGGGGTGAACAGGATTTCCGGGTGTCCATCCCAACGACCTGAAC 471  
 2y 483 ATTCAAAACTCGATGTGAGTGTGAGCTGTGCTGTGTGTGATCATTTCACTGG 540  
 Db 472 AAGATCTCAATTTGAGAGCAGCATCATCTTGTGCTTGTGGGGCATCATCTGTTG 529

RESULT 15  
 JS-09-944-807-20

Sequence 20, Application US/09944807  
 Patent No. US2002011949A1

GENERAL INFORMATION:

APPLICANT: Boehringer Ingelheim Pharma KG  
 TITLE OF INVENTION: Method for identifying substances which positively  
 TITLE OF INVENTION: influence inflammatory conditions of chronic  
 TITLE OF INVENTION: inflammatory airway diseases  
 FILE REFERENCE: 082.00n  
 CURRENT APPLICATION NUMBER: US/09/944,807  
 CURRENT FILING DATE: 2001-08-31  
 PRIOR APPLICATION NUMBER: UK 0021484.1  
 PRIOR FILING DATE: 2000-09-01  
 NUMBER OF SEQ ID NOS: 24  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 20  
 LENGTH: 2051

TYPE: DNA  
 ORGANISM: Homo sapiens  
 JS-09-944-807-20

Query Match  
 Best Local Similarity 7.7%; Score 82.8; DB 10; Length 2051;  
 Matches 186; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

2y 183 TTCTCGTGGGATTTCCAGGCAATGCAATGATGATTCACCTTACATTTTCAAAATGAGA 242  
 Db 172 TTATCTTTGGGCTTGGGCAATGGCTTGCCTGTGGATTTCTGTTCCACCTCAAG 231

Qy 243 CCTTGAAGAGCAGCACCACATCATATGCTGAACCTGGCTGACAGATCTGCTATCTG 302  
 Db 232 TCCTGGAATCCAGCCGGAATTTCTCTGTTCAACCTGAGAGTGAAGCTTCTACTGATC 291  
 Qy 303 ACCAGCTCCCTTCTCTGATTCATCTATGCAAGTGGCAAACTGGATTTTGGAGAT 362  
 Db 292 ATCTGCTGCGCTTGGATGAGTACTATATGCGGCTTCAAGTGAACCTTTGGGGAC 351  
 Qy 363 TTCATGTGATGATTTATCCGCTTCCAGCTTCCATTTCAACCTGTATAGAGCATCCTTTC 422  
 Db 352 ATCCCTTGGCCGCTGCTGCTTCTTATGTTGCCATGAAACCCGAGGAGCATCATCTTC 411  
 Qy 423 CTCACCTGTTTACGATCTTCCGCTACTGTGTGATCATTTACCCATGAGCTGCTTTTC 482  
 Db 412 CTCACGCTGTGGGGTGAACAGGATTTCCGGGTGTCCATCCCAACGACCTGAAC 471  
 Qy 483 ATTCAAAACTCGATGTGAGTGTGAGCTGTGCTGTGTGTGATCATTTCACTGG 540  
 Db 472 AAGATCTCAATTTGAGAGCAGCATCATCTTGTGCTTGTGGGGCATCATCTGTTG 529

Search completed: January 30, 2003, 06:50:14  
 Job time : 87 secs

TITLE OF INVENTION: Polypeptides  
 FILE REFERENCE: 799  
 CURRENT APPLICATION NUMBER: US/09/728,952  
 CURRENT FILING DATE: 2000-11-30  
 NUMBER OF SEQ ID NOS: 101  
 SOFTWARE: pf\_genes Version 2.0  
 SEQ ID NO 26

LENGTH: 1700  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (232)..(1272)  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(1700)  
 OTHER INFORMATION: n = a,t,c or g  
 US-09-728-952-26

Query Match 8.7%; Score 93.6; DB 10; Length 1700;  
 Best Local Similarity 52.3%; Pred. No. 1,1e-17;  
 Matches 207; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

2y 145 TCAGATGACCTACCTCCCTGTTATTTATGCAATTAATCTCTGCGGATTTCCAGGCA 204  
 |||||  
 Db 338 TCAGAGAGAAATTTTCCCAATGTATATCGATAATAATTTTCTGGGAGCTTGGGAA 397  
 2y 205 ATGACAGATGATATTCACATTAATTTCAAAATGAGACCTTGGAGAGCAGACCAATCA 264  
 |||||  
 Db 398 ATGGGTTTCCATATATATGTTTCTCGACGCTTATPAGAGCTTCATCTGTAAACGTTT 457  
 2y 265 TTATGTGTAACCTGCGCTGACAGATCTGTATCTGACAGGCTCCCTCCCTGATTC 324  
 |||||  
 Db 458 TCATGTAAATCTGGCATTTTCAGATCTCCGTTCATAGAGACGCTTCCCTTACGGGCTG 517  
 2y 325 ACTACTATGCGCAGTGGCGAAATCTGATCTTTGAGATTGATGTAAAGTTTATCCGCT 384  
 |||||  
 Db 518 ACTATTATCTTAAGAGGCTCCCAATGATATTGGAGACCTGCGCTGACGAGATTATGCTT 577  
 2y 385 TCAGCTTCATTTCAACCTGTATAGAGACATCCCTTCCCTGACCTGTTTCCAGATTTCC 444  
 |||||  
 Db 578 ATTCCTTGATATGTCATATGACAGAGATTTATTTCTGACCGTGTGATGTGTC 637  
 2y 445 GCTACTGTGTATCATTCACCCCAATGAGCTGCTTTCCATTCACAAAACCTGATGTGAG 504  
 |||||  
 Db 638 GTTCTCGGAATGTTTCAACCCCTTTGGGCTTCTGCAATGACACGATCAGAGAGTGCCT 697  
 2y 505 TTGTAGCTGTGCTGTGTGTGTGATCATTTTCACTGG 540  
 |||||  
 Db 698 GATCCTCTGTGGGATCATATGATCCTTATCATGG 733

RESULT 11  
 JS-09-788-133-1  
 Sequence 1, Application US/09788133

Patent No. US20020052001A1

GENERAL INFORMATION:

APPLICANT: GLAXO GROUP LTD

TITLE OF INVENTION: ASSAY

FILE REFERENCE: P79011

CURRENT APPLICATION NUMBER: US/09/788,133

CURRENT FILING DATE: 2001-02-20

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 1020

TYPE: DNA

ORGANISM: homo sapiens

FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (1)..(1020)

JS-09-788-133-1

Query Match 8.4%; Score 90.8; DB 10; Length 1020;

Best Local Similarity 47.7%; Pred. No. 5.9e-17;  
 Matches 309; Conservative 0; Mismatches 327; Indels 12; Gaps 1;

Qy 183 TTCCCTGGGATTTCCAGGCAATGCACTAGTATATCCACTTACATTTTCAAAATAGA 242  
 |||||  
 Db 124 TTATACCTGGCTTTAGTTGGCAATACCTGGCTCTGTGGCTTTTATCCAGACCAAG 183  
 Qy 243 CTTTGAAGACAGACCATCATTTATGCTGAACCTGGGCTGACAGATCTGCTATCTG 302  
 |||||  
 Db 184 TCCGGACCCCGGCAAGTGTCTCTGATGATCTGCGCGGCGCATTTGCTGCGGTG 243  
 Qy 303 ACCAGCTCCCTTCTGATTCATTAATGCAAGTGGGAAATCTGATCTTTGGAGAT 362  
 |||||  
 Db 244 CTGGTCTGCGCCACCCGCTGCTGTACCACTTCTTGGGAACACTGGCCATTTGGGAA 303  
 Qy 363 TTCAATGTAAAGTTTATCCGTTTCAAGCTTCAATTTCAACCTGTATAGAGATCTCTTC 422  
 |||||  
 Db 304 ATGCAATGCGCTACACCGGCTTCTTCTTACCTCAACATGATGCGCAGATCTAATTC 363  
 Qy 423 CTCACCTGTTTCAAGATCTTCCGCTACTGTGTATCAATTCACCAATGAGCTTTTCC 482  
 |||||  
 Db 364 CTCACCTGATACAGCGCGACCGTTTCTGACATTTGTGACCCGCTCAAGTCCCTCAAG 423  
 Qy 483 ATTCAAAAATCTGATGTGCAATTTAGCTGTGCTGTGTGTGATCATTTCACTGTA 542  
 |||||  
 Db 424 CTCGCAAGGCCCTCTAGCAACACTGCGCTGTGCTTCTCTGTGGTGTGTGTGCTGTG 483  
 Qy 543 GCTGTATTCGATGACCTTTTATATCAATCAACCAAGACCAAGATCAAGCTGT 602  
 |||||  
 Db 484 GCAATGCGCCGCTGCTGTGTGAGCCCAAGACCGTGCAGAACCAACAGGTGTGTGC 543  
 Qy 603 CTGACCTCAACAGTTGGATGAATCAATATTAAGTGTACACCTGATTTTGAAT 662  
 |||||  
 Db 544 CTGAGCTGTACCGGAAAGGCTCCACCATGC-----CTGTGTGCTGTG 591  
 Qy 663 GCAACTACTTCTCTCTCCCTTGTGTATGATGACACTTTGCTATACCATTTATCCAC 722  
 |||||  
 Db 592 GCAATGCGCTTCACTTCCGTTTATCAACAGGTCACAGCTGTACCTGTATCATCCGC 651  
 Qy 723 ACTTGACCAATGACATGCAATGACAGCTGCTTTAAGCAAGAAAGCAGAAAGCTAAC 782  
 |||||  
 Db 652 AGCTTGGGCGAGGCGCTGCTGTGTGAGAGAGCGCTCAAGACCAAGGCGATGATG 711  
 Qy 783 ATTCGCTACTCTGTGATTTTATGTAATTTTATCCCTTCAATTC 830  
 |||||  
 Db 712 GCCAATGCTGCGCATTTCTGCTGTGCTGTGCTTGTGCTTACACAGCTC 759

RESULT 12  
 US-09-880-107-2143  
 Sequence 2143, Application US/09880107

Patent No. US20020142981A1

GENERAL INFORMATION:

APPLICANT: Horne, Darci T.

APPLICANT: Vockley, Joseph G.

APPLICANT: Scherf, Uwe

TITLE OF INVENTION: Gene Logic, Inc.

FILE REFERENCE: 44921-5028-WO

CURRENT APPLICATION NUMBER: US/09/880,107

CURRENT FILING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR FILING DATE: 2000-06-14

PRIOR APPLICATION NUMBER: US 60/237,054

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2143

LENGTH: 1670

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:  
 OTHER INFORMATION: Genbank Accession No. US20020142981A1 L06797

APPLICANT: Pfizer Inc  
TITLE OF INVENTION: No. US20010039037A1el Polypeptide  
FILE REFERENCE: PC10914ADAM  
CURRENT APPLICATION NUMBER: US/09/826,791  
CURRENT FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 0008504.3  
PRIOR FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: 60/198,367  
PRIOR FILING DATE: 2000-04-19  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 993  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-826-791-1

Query Match  
Best Local Similarity 52.3%; Score 93.6; DB 10; Length 993;  
Matches 207; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

Qy 145 TCAAGATGCACTACCTCCCTGTTATTATGACATTATCTCTCGTGGATTTCCAGCA 204  
Db 59 TCAAGAGAGATTTTCCCAATTTGATATCTGATTAATTTTCTGGGAGTCTTGGGA 118  
Qy 205 ATGAGTAGATGATTCACCTTATCAATTTTCAAAATGAGACCTTGGAGAGACACATCA 264  
Db 119 ATGGGTGTCATATATGTTTCTGACGCTTATTAAGATCCACATCTGTGAACCTTT 178  
Qy 265 TTATGCTGAACCTGCGCTGACAGATCTGCTGATCTGACACGCTCCCTCTGATTC 324  
Db 179 TCATGCTAAATCTGGCCATTTGAGATCTCTGTTCAATTAACAGGCTTCCCTTACGGCTG 238  
Qy 325 ACTACATGCGAGTCCGAGAACTGATCTTTGAGATTTCATGTTAGTTATTCGCT 384  
Db 239 ACTATATCTTGAAGGCTCCCAATTTGATTTTGGAGACCTGCGCTGAGATTAATGCTT 298  
Qy 385 TCAGCTTCATTTCAACCTGATATAGAGACATCTCTTCCACCTGTTTCAGATCTTCC 444  
Db 229 ATTCCTGATATCAACATGATACAGATATTTATTTCCGACCGTGTGAAGTGTGTC 358  
Qy 445 GCTACTGTGTGATCAATTCACCAATGAGCTGCTTTTCATTCACAAACTCGATGTGAC 504  
Db 359 GTTTCCTGGCAATGTTGACCCCTTCCGCTTGTGATGTACACACATCAGAGATGCTT 418  
Qy 505 TTGTAGCTGTCTGCTGTGGTGTGATATTTCACTGG 540  
Db 419 GGATCTCTGTGGATCAATATGATCTTATCATGG 454

RESULT 6  
US-09-826-478-1

Sequence 1, Application US/09828478  
Patent No. US2002015528A1  
GENERAL INFORMATION:  
APPLICANT: Xiao, Yonghong  
TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR  
FILE REFERENCE: 04974.00458  
CURRENT APPLICATION NUMBER: US/09/828,478  
PRIOR FILING DATE: 2001-04-09  
PRIOR APPLICATION NUMBER: 60/195,196  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: 60/254,876  
PRIOR FILING DATE: 2000-12-13  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 1041  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-826-478-1

Query Match  
Best Local Similarity 52.3%; Score 93.6; DB 9; Length 1041;  
Matches 207; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

Qy 145 TCAAGATGCACTACCTCCCTGTTATTATGACATTATCTCTCGTGGATTTCCAGCA 204  
Db 107 TCAAGAGAGATTTTCCCAATTTGATATCTGATTAATTTTCTGGGAGTCTTGGGA 166  
Qy 205 ATGAGTAGATGATTCACCTTATCAATTTTCAAAATGAGACCTTGGAGAGACACATCA 264  
Db 167 ATGGGTGTCATATATGTTTCTGACGCTTATTAAGATCCACATCTGTGAACCTTT 226  
Qy 265 TTATGCTGAACCTGCGCTGACAGATCTGCTGATCTGACACGCTCCCTCTGATTC 324  
Db 227 TCATGCTAAATCTGGCCATTTCAAGATCTCTGTTCAATTAACAGGCTTCCCTTACGGCTG 286  
Qy 325 ACTACTATGCAATGCGGAGAACTGATCTTTGAGATTTCATGTTAGTTATTCGCT 384  
Db 287 ACTATATCTTGAAGGCTCCCAATTTGATTTTGGAGACCTGCGCTGACAGATTAATGCTT 346  
Qy 385 TCAGCTTCATTTCAACCTGATATAGAGACATCTCTTCCACCTGTTTCAGATCTTCC 444  
Db 347 ATTCCTGATATGCAACATGATACAGATATTTATTTCTGACCGCTGAGTGTGTC 406  
Qy 445 GCTACTGTGTGATCATTCACCAATGAGCTGCTTTTCATTCACAAACTCGATGTGAC 504  
Db 407 GTTTCCTGGCAATGTTGACCCCTTCCGCTTGTGATGTACACAGATCAGAGATGCTT 466  
Qy 505 TTGTAGCTGTCTGCTGTGGTGTGATATTTCACTGG 540  
Db 467 GGATCTCTGTGGATCAATATGATCTTATCATGG 502

RESULT 7  
US-09-826-791-5

Sequence 5, Application US/09826791  
Patent No. US20010039037A1  
GENERAL INFORMATION:  
APPLICANT: Pfizer Inc  
TITLE OF INVENTION: No. US20010039037A1el Polypeptide  
FILE REFERENCE: PC10914ADAM  
CURRENT APPLICATION NUMBER: US/09/826,791  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 0008504.3  
PRIOR FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: 60/198,367  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 1041  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1041)  
US-09-826-791-5

Query Match  
Best Local Similarity 52.3%; Score 93.6; DB 10; Length 1041;  
Matches 207; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

Qy 145 TCAAGATGCACTACCTCCCTGTTATTATGACATTATCTCTCGTGGATTTCCAGCA 204  
Db 107 TCAAGAGAGATTTTCCCAATTTGATATCTGATTAATTTTCTGGGAGTCTTGGGA 166  
Qy 205 ATGAGTAGATGATTCACCTTATCAATTTTCAAAATGAGACCTTGGAGAGACACATCA 264  
Db 167 ATGGGTGTCATATATGTTTCTGACGCTTATTAAGATCCACATCTGTGAACCTTT 226  
Qy 265 TTATGCTGAACCTGCGCTGACAGATCTGCTGATCTGACACGCTCCCTCTGATTC 324  
Db 227 TCATGCTAAATCTGGCCATTTCAAGATCTCTGTTCAATTAACAGGCTTCCCTTACGGCTG 286





475 TCCTACACCTTACATGCAACAACTGGGTCTACGGGAGGCCCTTGACAGGTGCTATT 534  
384 TTACAGCTTCATTTCAACCTGTATAGCAGCATCTCTTCTCACTGTTTCAAGATCTTC 443  
535 GGCCTTTTCTATAGTAACATGTAATGCTCATCTCTTATGACCTGCTCAGGTGCAAG 594  
444 CGCTACTGTGTATCATTCACCAATGAGCTGCTTTTCCATTCAAAAACCTCGATGTGCA 503  
595 AGGTACTGGGTATCGTGAACCCCATGAGGACACCCGAGAAAGGCAACATGCGCGTT 654  
504 GTTGTAGCTGTGCTGTGTGTGATCATTTCACTGTGTAAGTCTGTC 548  
655 GCGCTCTCTTGGCAATCTGCTCTGATTTTCTGTGTACCATTC 699

RESULT 15  
US-08-472-840-60  
Sequence 60, Application US/08472840  
Patent No. 5763575  
GENERAL INFORMATION:  
APPLICANT: SUNDELIN, JOHAN  
APPLICANT: SCARBOROUGH, ROBERT M.  
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS  
TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,840  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,301  
FILING DATE: 25-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: ADLER, REID G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: 2803-0006.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 60:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2732 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 73..1269  
US-08-472-840-60

Query-Match 9.0%; Score 97.8; DB 1; Length 2732;  
Best Local Similarity 52.6%; Pred. No. 6e-20;  
Matches 213; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

2y 144 CTAAAGATGCACTTCCCTGTTATTTATGCAATATCTTCTGTTGGATTTCCAGGC 203  
2b 295 CTGACCAAGGCTCTTCCGCTGCTACATTAATGTTGTGATGTTGCTTGGCCAGT 354  
2y 204 AATGCAATAGATATCCACTTACATTTCAAAATGAGACCTTGAAGAGACGACCATC 263

Db 355 AATGGATGGCCCTCTGGAATCTTCTTTCCGAACGAAAGAAACACCCCGCGTATT 414  
Qy 264 AATATGCTGAACCTGGCTGACAGATCTGCTATGTACCGAGCTTCCCTTCTTATT 323  
Db 415 TACATGGCAACCTGGGCTTGGCCGACCTCTCTGTCATCTGTGTTCCCTGAAATC 474  
Qy 324 CACTACTATGCCAGTGGCCGAAACCTGATCTTGAAGATTCAATGTGTAATATCGC 383  
Db 475 TCCTACACCTTACATGCAACAACTGGGTCTACGGGAGGCCCTTGACAGGTGCTATT 534  
Qy 384 TTACAGCTTCATTTCAACCTGTATAGCAGCATCTCTTCTCACTGTTTCAAGATCTTC 443  
Db 535 GGCCTTTTCTATAGTAACATGTAATGCTCATCTCTTCACTGACCTGCTCAGGTGCAAG 594  
Qy 444 CGCTACTGTGTATCATTCACCAATGAGCTGCTTTTCCATTCAAAAACCTCGATGTGCA 503  
Db 595 AGGTACTGGGTATCGTGAACCCCATGAGGACACCCGAGAAAGGCAACATGCGCGTT 654  
Qy 504 GTTGTAGCTGTGCTGTGTGTGATCATTTCACTGTGTAAGTCTGTC 548  
Db 655 GCGCTCTCTTGGCAATCTGCTCTGATTTTCTGTGTACCATTC 699

Search completed: January 30, 2003, 06:48:46  
Job time : 78 secs

Sequence 1, Application US/08476976  
Patent No. 5874400  
GENERAL INFORMATION:  
APPLICANT: SUNDELIN, JOHAN  
APPLICANT: SCARBOROUGH, ROBERT M.  
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS  
AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,976  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/390,301  
FILING DATE: 25-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: ADLER, REID G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: 2803-0006.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1475 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 232..1416  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 232  
US-08-476-976-1

Query Match 9.0%; Score 97.8; DB 2; Length 1475;  
Best Local Similarity 52.6%; Pred. No. 4.3e-20;  
Matches 213; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

QY 144 CTCAGATGCACTACCTCCGTTATTTATGACATTAATCTTCCTCGGGATTTCCAGGC 203  
DB 442 CTGACCAAGGCTTTCTCCGGTGTCTACATTAATGTTGTGATGTTGCTTCCAGT 501  
QY 204 AATGCAATGATGATTCATTAATTTTCAAAATGAGACCTTGAGAGAGACGACCATC 263  
DB 502 AATGGCAATGGCCCTCTGGATCTTCCTTTCCGAGAGAGAAACACCCCGCGTGATT 561  
QY 264 AATATGCTGAACCTGGCGCTGACAGATCTGTATCTGACCAAGCTCCCTTCTGATT 323  
DB 562 TACTATGGCCAACTGGGCGCTTGGCGACCTCTCTGTGATCTGTGTTCCCTCGAAGATC 621  
QY 324 CACTACTATGCACTGAGGAGAACTGATCTTTGGAGATTCATGTAAGTTATCCGC 383  
DB 622 TCTACACCACTATACGACACACTGGGTCTAAGGGAGGCCCTGTGCAAGTGTCTATT 681  
QY 384 TTGAGCTTCAATTTCAACTGTATAGACAGATCCCTCTCACTGTTTGAAGATCTTC 443  
DB 682 GGGCTTTTCTATGATATCATATATGTCATCTCTTCAATGACCTGCGCTGAG 741

QY 444 CGCTACTGTGTGATCATTCACCCATGAGTGTCTTTTCATTCACAAACTCGATGCA 503  
DB 742 AGGTACTGTGTGATCATTCACCCATGAGTGTCTTTTCATTCACAAACTCGATGCA 801  
QY 504 GTTGAGCTGTGTGATCATTCACCCATGAGTGTCTTTTCATTCACAAACTCGATGCA 548  
DB 802 GGGCTTTTCTATGATATCATATATGTCATCTCTTCAATGACCTGCGCTGAG 846

RESULT 12  
US-08-474-410-1  
Sequence 1, Application US/08474410  
Patent No. 6043212  
GENERAL INFORMATION:  
APPLICANT: SUNDELIN, JOHAN  
APPLICANT: SCARBOROUGH, ROBERT M.  
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS  
AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,410  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/390,301  
FILING DATE: 25-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: ADLER, REID G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: 2803-0006.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1475 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 232..1416  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 232  
US-08-474-410-1

Query Match 9.0%; Score 97.8; DB 3; Length 1475;  
Best Local Similarity 52.6%; Pred. No. 4.3e-20;  
Matches 213; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

QY 144 CTCAGATGCACTACCTCCGTTATTTATGACATTAATCTTCCTCGGGATTTCCAGGC 203  
DB 442 CTGACCAAGGCTTTCTCCGGTGTCTACATTAATGTTGTGATGTTGCTTCCAGT 501  
QY 204 AATGCAATGATGATTCATTAATTTTCAAAATGAGACCTTGAGAGAGACGACCATC 263  
DB 502 AATGGCAATGGCCCTCTGGATCTTCCTTTCCGAGAGAGAAACACCCCGCGTGATT 561  
QY 264 AATATGCTGAACCTGGCGCTGACAGATCTGTATCTGACCAAGCTCCCTTCTGATT 323

TELEFAX: 617-523-6440  
INFORMATION FOR SEQ ID NO: 370:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1020 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 28..1011  
US-08-513-9748-370

Query Match 9.3%; Score 100; DB 3; Length 1020;  
Best Local Similarity 57.5%; Pred. No. 7.3e-21;  
Matches 200; Conservative 0; Mismatches 145; Indels 3; Gaps 1;

2y 270 CTGACCTGGCTGACAGATCTGCTATCTGACAGCCCTCCCTTCCTGATTCATC 329  
Db 223 CTGACCTGGCTGACAGATCTGCTATCTGACAGCCCTCCCTTCCTGATTCATC 282  
2y 330 TATGCCAGTGGCCAAAATCTGATTTTGAGATTTCATGTGAATTATCCGCTTACG 389  
Db 283 TAGCCAGAGGGGACCACTGGCCCTTGGAGACCTGGCTCCGCTTGTAGCTTCTC 342  
2y 390 TTCCATTTCACCTGTATAGAGATCTCTCTCACTGTTTACAGATCTCCGCTAC 449  
Db 343 TTCTATGCCAATCTACATGAGAGATCTCTCTCACTGATTCATTCAGAGCTAC 402  
2y 450 TGTGTATCATTCACCAATAGAGCTGCTTTTCATTCACAAATCTCATGTGAGTT 506  
Db 403 CTGGGATCTGCCACCCCTGGCTTCTCTGACAGAGGTGGAGGTGGCGGTGCTGG 462  
2y 507 GTAGCTGTCTGTGTGTGTGATTCATTCAGTGTAGCTGTATTCGATGACCTTCTG 566  
Db 463 GTAGTGTGTGAGT 522  
2y 567 ATGACATCAACCAAGAGACCAAGATCAAGCTGTCTGACCTCACC 614  
Db 523 GCTGCCAGGCAATCCAGCGACGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 570

RESULT 8  
US-08-097-938-1

Sequence 1, Application US/08097938  
Patent No. 5629174

GENERAL INFORMATION:  
APPLICANT: SUNDELIN, JOHAN  
APPLICANT: SCARBOROUGH, ROBERT M.  
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR AND ITS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20006-1812

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/097,938  
FILING DATE: 26-JUL-1993  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 22803-20006.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SRO ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1475 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 232..1416  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 232  
US-08-097-938-1

Query Match 9.0%; Score 97.8; DB 1; Length 1475;  
Best Local Similarity 52.6%; Pred. No. 4.3e-20;  
Matches 213; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

Qy 144 CTGAAGATGACCTACCTCCCTGTTATTTATGCAATTCCTTCCTGCGGATTTCCAGGC 203  
Db 442 CTGACCAAGGCTTCTTCCGGTGTCTACATTTGTGTGTGATTTGTTGCTTCCAGT 501  
Qy 204 AATGACAGTATGATATCACTTATTCATTTTGAATGAGACCTTGAAGAGACACCATC 263  
Db 502 AATGACATGCGCTCTGATCTTCTTTCCGAGAGAAAGAAACCCCGCTGATT 561  
Qy 264 ATTATGCTGAACTGCGCTGACAGATCTGCTATCTGACAGACCTCCCTCTGATT 323  
Db 562 TACATGGCAACCTGGCTTGGCGGACCTCTCTGTGATCTGTGTTCCCTTAAGATC 621  
Qy 324 CACTATATGCACTGCGGAAATCTGATCTTTGGAATTCATGTGTATTCGCG 383  
Db 622 TCTTACCACTTACATGCACTGCGGTCTACCGGAGGCGCTGTGCAAGTCTCAT 681  
Qy 384 TTGAGCTTCACTTCACTGATATGAGACATCTCTTCTCACTGTTTACGATCTTC 443  
Db 682 GGGCTTTCTATGATGATATGATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 741  
Qy 444 CGTACTGTGTATCATTCACCAATAGAGCTGCTTTTCATTCACAAATCTCATGTGCA 503  
Db 742 AGTACTGGGTGATCGTGAACCCATGGACACCCAGAGAGGCAATGCGCTT 801  
Qy 504 GTTGTAGCTGT 548  
Db 802 GGGCTTCTTGGCAATCTGGCTCTGATTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 846

RESULT 9  
US-08-476-000-1

Sequence 1, Application US/08476000  
Patent No. 5716789

GENERAL INFORMATION:  
APPLICANT: SUNDELIN, JOHAN  
APPLICANT: SCARBOROUGH, ROBERT M.  
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006-1812

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,000



Db 649 GCAACTTGCAAAAAGCTGGCTGGGAGAGAGGCTGCCGTAAGAAAGTACTACTTTCATT 708  
 Qy 168 ATTATGAGCAATTAATCTTCTCGTGGGAAATTCAGAGCAATGAGATGATTCACATTAC 227  
 Db 709 TTTTATGGGATGATGCTGTTGGGAGCTCTTGAAATACATTTGTTGTTAGGGCTAC 768  
 Qy 228 ATTTTCAAAATGAGACCTTGGAGAGAGAGCAACCATTAATGATGAACTGGCCGTGACA 287  
 Db 769 ATCTTCTCTCTGAAAGAACTGGAGAGAGATTAATTAATCTTTAACTCTGCTCTCT 828  
 Qy 288 GATCTGCTGATATGAGACAGACCTCCCTCTCTGATTAACAATGACAGAGGAGAAAC 347  
 Db 829 GACTTACCTTTCTGTCGACACCTCCCATGCTGATTAAGAGATTAATGCAATG---AAAC 885  
 Qy 348 TGGATCTTTGGAGATTTCAATGTGTAAGTTATTCGGCTTACCTTCAATTCACCTGAT 407  
 Db 886 TGGATATATGAGACGCTGCTGATTAAGCAACGATATGCTTCAATGCAACCTCTAT 945  
 Qy 408 AGAGATCTCTTCTCCGACCTGTTTGAAGATCTTCGGCTAATGATGATCAATCCCA 467  
 Db 946 ACCAGATCTCTCTTCTGCACTTTATGATGATGATGATGATGATGATGATGATGAT 1005  
 Qy 468 ATGAGCTGCTTTTCATTCACAAAAGCTGATGATGATGATGATGATGATGATGATGAT 527  
 Db 1006 TTCCGAGAAACACCTTCTGCAAAAGAAAGATTTCTATTTTAACTCTTGGCCATTGG 1065  
 Qy 528 ATCAATTCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 587  
 Db 1066 GTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1125  
 Qy 588 AACAGATCAGCTGCTGCTGACCTTCAACGATTTGGATGAATCAATTAATTAAGTGAT 647  
 Db 1126 AAGGAGACCACTGATATGATTTTGAAGATTTGCAAGCTTGAAGACCCCACTAACCTGAT 1185  
 Qy 648 AACCTGATTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 707  
 Db 1186 AGCATGCTTAAACCTGTTGGGGCTCTTAATCTCTTTTGAATGATGATGATGAT 1245  
 Qy 708 ACCAGATTTT-----ATCCACACTCTGACCCATGAGATGACAGCTGCTTAAG 761  
 Db 1246 TACAGATGCTCTCTCTCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1305  
 Qy 762 CAGAAAGCAGAGAGCTTAACATTTCTGCTACTCTTGCATTTTAAAGTATTTTAAACC 821  
 Db 1306 GAAAGGCTCTCAACTTGTGATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1365  
 Qy 822 TTCCATATCTTGAAGGCTGATTCGATGAGATGATGATGATGATGATGATGATGAT 860  
 Db 1366 TATCAGCTCATGCGGAATGAGAGATGATGATGATGATGATGATGATGATGATGAT 1404

result 2  
 JS-08-749-707-1  
 Sequence 1, Application US/08749707

Patent No. 6063582  
 GENERAL INFORMATION:  
 APPLICANT: Conley, Pamela B.  
 APPLICANT: Jantzen, Hans-Michael  
 TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP  
 STREET: 1800 M Street, N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20036-5869  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/749,707  
 FILING DATE: 15-NOV-1996  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Adler, Reid G.  
 REGISTRATION NUMBER: 30,988  
 REFERENCE/DOCKET NUMBER: 04481-5010-01-US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-467-7000  
 TELEFAX: 202-467-7176  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1996 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 625..1626  
 US-08-749-707-1  
 Query Match 11.9%; Score 129; DB 3; Length 1996;  
 Best Local Similarity 50.1%; Pred. No. 1.4e-29;  
 Matches 380; Conservative 0; Mismatches 370; Indels 9; Gaps 2;

Qy 108 GCTGCTTTTGGAAATTCATGATGAAACATCCACTCAAGATGCACTACCTCCCTGTT 167  
 Db 649 GCAACTTGCAAAAAGCTGGCTGGGAGAGAGGCTGCCGTAAGAAAGTACTACTTTCATT 708  
 Qy 168 ATTATGAGCAATTAATCTTCTCGTGGGAAATTCAGAGCAATGAGATGATTCACATTAC 227  
 Db 709 TTTTATGGGATGATGCTGTTGGGAGCTCTTGAAATACATTTGTTGTTAGGGCTAC 768  
 Qy 228 ATTTTCAAAATGAGACCTTGGAGAGAGAGCAACCATTAATGATGAACTGGCCGTGACA 287  
 Db 769 ATCTTCTCTCTGAAAGAACTGGAGAGAGATTAATTAATCTTTAACTCTGCTCTCT 828  
 Qy 288 GATCTGCTGATATGAGACAGACCTCCCTCTCTGATTAACAATGACAGAGGAGAAAC 347  
 Db 829 GACTTACCTTTCTGTCGACACCTCCCATGCTGATTAAGAGATTAATGCAATG---AAAC 885  
 Qy 348 TGGATCTTTGGAGATTTCAATGTGTAAGTTATTCGGCTTACCTTCAATTCACCTGAT 407  
 Db 886 TGGATATATGAGACGCTGCTGATTAAGCAACGATATGCTTCAATGCAACCTCTAT 945  
 Qy 408 AGAGATCTCTTCTCCGACCTGTTTGAAGATCTTCGGCTAATGATGATCAATCCCA 467  
 Db 946 ACCAGATCTCTCTTCTGCACTTTATGATGATGATGATGATGATGATGATGATGAT 1005  
 Qy 468 ATGAGCTGCTTTTCATTCACAAAAGCTGATGATGATGATGATGATGATGATGATGAT 527  
 Db 1006 TTCCGAGAAACACCTTCTGCAAAAGAAAGATTTCTATTTTAACTCTTGGCCATTGG 1065  
 Qy 528 ATCAATTCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 587  
 Db 1066 GTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1125  
 Qy 588 AACAGATCAGCTGCTGCTGACCTTCAACGATTTGGATGAATCAATTAATTAAGTGAT 647  
 Db 1126 AAGGAGACCACTGATATGATTTTGAAGATTTGCAAGCTTGAAGACCCCACTAACCTGAT 1185  
 Qy 648 AACCTGATTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 707  
 Db 1186 AGCATGCTTAAACCTGTTGGGGCTCTTAATCTCTTTTGAATGATGATGATGAT 1245  
 Qy 708 ACCAGATTTT-----ATCCACACTCTGACCCATGAGATGACAGCTGCTTAAG 761  
 Db 1246 TACAGATGCTCTCTCTCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1305  
 Qy 762 CAGAAAGCAGAGAGCTTAACATTTCTGCTACTCTTGCATTTTAAAGTATTTTAAACC 821  
 Db 1306 GAAAGGCTCTCAACTTGTGATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1365



M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. *Genome Res.* 10 (10), 1617-1630 (2000)  
 wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,  
 Wachihi, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga,  
 S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and  
 Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multichannel sequencer. *Genome Res.*  
 10 (11), 1757-1771 (2000)  
 Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara,  
 Y. and Hayashizaki, Y.  
 Computer-based methods for the mouse full-length cDNA  
 encyclopedias: real-time sequence clustering for construction of a  
 nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)  
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
 further details.  
 e mouse tissues.

# FEATURES

## source

1. 422  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone="F530201F11"  
 /clone\_lib="RIKEN full-length enriched, adult male kidney"  
 /sex="male"  
 /tissue\_type="kidney"  
 /dev\_stage="adult"  
 /lab\_host="SOLR"  
 /note="Site 1: XhoI; Site 2: SstI; cDNA library was  
 prepared and sequenced in Mouse Genome Encyclopedia  
 Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in  
 RIKEN. Division of Experimental Animal Research in Riken  
 contributed to prepare mouse tissues. 1st strand cDNA was  
 primed with a primer 15'  
 GAGGAGAGAGCGCGCGCACTCTTTTCTTTTCTTTT 3'. cDNA was  
 prepared by using trehalose thermo-activated reverse  
 transcriptase and subsequently enriched for full-length by  
 cap-trapper. Second strand cDNA was prepared with the  
 primer adapter of sequence 15'  
 GAGGAGAGAGAGATCCAGATCTCAATTAATTAATTAACCCCCCCC 3'.  
 cDNA was cleaved with XhoI and SstI."  
 BASE COUNT 104 a 100 c 88 g 130 t  
 ORIGIN

Query Match 9.3%; Score 100; DB 10; Length 422;  
 Best Local Similarity 57.5%; Pred. No. 1.2e-17;  
 Matches 200; Conservative 0; Mismatches 145; Indels 3; Gaps 1;

112 CTTTGAATGACCTGATGAATAATCCACTCAAGATGACCTCCCTGTTATTT 171  
 75 CTTGAGAAATGGTTGGCAACAGAGGCTATCTGAATAAGTACTCTCGCATTTT 134  
 172 ATGCAATATCTTCTCGTGGGATTTTCAGCAATGAGTATTCACCTTACATTT 221  
 135 ATGCAATGAGTTCAATTTTGGAGCTTGGGATGATCACTGATGTTGGCTACTCT 194  
 232 TCAAAATGAGACCTTGAAGAGAGACCATCATATATGCTGAACCTGGCTGCACAGATC 291  
 195 TCTGATGAAAGACCTGGAACAGAGCAATGTCTATCTTTTAACTTTTCATCTGACT 254  
 292 TGTCTATCTGACAGAGCTCCCTCTGATTCATCACTATGACAGTGGGAAACCTGGA 351  
 255 TTGCTTCTGTCGACCTCTCCATCTGATTAAGATTAAGCAAT--GATTAAGGGA 311  
 352 TCTTGGAGATTCATGTAAGTTATTCGCTTCAGCTTCAATTTCAACCTGATAGCA 411  
 312 CTTATGGAATGTTCTCTGATTAAGCAACGATATGCTTCAACCAACTCTACACCA 371  
 412 GCATCTCTTCTCTACCTGTTTCAGATCTTCGCTACCTGATGATCA 459  
 372 GCATCTCTCTCTCACTTCATTAAGATGAGCAGATATCTGTCATCA 419

RESULT 14  
 BG924078 801 bp mRNA linear EST 05-JUN-2001  
 LOCUS 60282365F1 NCI\_CGAP\_Mam6 Mus musculus cDNA clone IMAGE:4952433 5',  
 DEFINITION mRNA sequence.

ACCESSION BG924078  
 VERSION BG924078.1 GI:14304554  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus.

REFERENCE  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
 Tissue Procurement: Jeffrey Green M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
 Plate: LLAM10910 row: e column: 10  
 High quality sequence start: 25  
 High quality sequence stop: 799.

# FEATURES

## source

1. 801  
 /organism="Mus musculus"  
 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:4952433"  
 /clone\_lib="NCI CGAP Mam6"  
 /sex="Female, virgin"  
 /tissue\_type="infiltrating ductal carcinoma"  
 /dev\_stage="5 months"  
 /lab\_host="DH10B"  
 /note="Organ: mammary; Vector: PCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
 Library constructed by Life Technologies. Investigator  
 providing samples: Jeffrey Green, M.D., NIH"  
 BASE COUNT 166 a 228 c 193 g 213 t  
 ORIGIN

Query Match 9.2%; Score 99.6; DB 13; Length 801;  
 Best Local Similarity 53.3%; Pred. No. 2e-17;  
 Matches 210; Conservative 0; Mismatches 184; Indels 0; Gaps 0;

155 CTACCTCCCTGTTATTTATGACATTAATCTTCTCGTGGGATTTCCAGCAATGACAGT 214  
 188 CTTTCTCCGCTGCTCACTATTAATGTTGATTTGATTTGGTCCCATGATGACATGCG 247  
 215 GATATCCACTTAATTTTCAAAATGAGACCTTGAAGAGAGACCATCATTAATGCGAA 274  
 248 CTTCTGATTTCTCTTTTCCGAAGAAAGAAACACCCCGGTGATTAACATGAGCCAA 307  
 275 CTTGCGCTGACAGATCTGCTATCTGACACAGCTCCCTCTGATTCATCACTATGCG 334  
 308 CTTGCGCTTGGCTGACCTCTCTGTCATCTGTTCCCTGCGCATTTGCTTCACT 367  
 335 CAGTGGGAAACCTGATCTTTGAAGATTCATGATGATTAATTCGCTTCACTTCA 394  
 368 ACATGGCAACACTGGGCTATGAGGAGCGCTGTGCAAGTGTCTATTGGCTTTTCTA 427  
 395 TTTCACCTGTATAGAGACATCTCTTCTCACTGTTTATAGATCTTCCGCTACTGT 454  
 428 TGGCAACATGATTTGCTTCATCTCTTCATGACCTGCTCAGGCTGACAGTACTGGGT 487  
 455 GATCATTCACCAATAGAGCTTTTCCATTCACAAAACTCGATGTCAGTGTAGCTG 514

and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence 15',  
 GAGAGAGATTCGAGTTAATTAATATCCCCCCCCCC 3'). cDNA was cleaved with BamHI and XhoI. Vector: a modified phluescript KS(+) after bulk excision from Lambda FLX I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.

## FEATURES

source  
 location/Qualifiers  
 1. 2542  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="FANTOM\_DB:5430432J15"  
 /db\_xref="MGI:1897121"  
 /db\_xref="taxon:10090"  
 /clone="5430432J15"  
 /tissue\_type="head"  
 /clone\_id="Riken full-length enriched mouse cDNA library"  
 /dev\_stage="6 days neonate"  
 1. 2542  
 /gene="P2ry2"  
 484..1605  
 /gene="P2ry2"  
 /note="data source:MGI, source key:MGI:105107, evidence:ISS  
 putative receptor P2Y, G-protein coupled 2 putative"  
 /codon\_start=1  
 /protein\_id="BAB30719.1"  
 /db\_xref="GI:12856589"  
 /db\_xref="MGI:105107"  
 /translation="MAADLEPNASTNGTMEGBELGYKCFNEDFKVLLPVSGYVC  
 VGLCLNVALYIFLCRTKMASTTYMFLAVSDSLVYASLLVLYVARGHMPSS  
 TVLCKLRFLEFYNLCSTILFCISVHRCGLRPHSRGRARARAAVAVVYL  
 VLAQCPVLYFTTYSVGRTRITCHDTSARLFSHPVAVSSVMGLLEPAVPSVILCY  
 VLMARLLPAGVTGSLPARKRSVTTALVAVPALCPPLHRTLLYSRSLDL  
 SCHTLVAIMAVYKTRPLASNSCLDPVLFLAGOLVRFARAKAPTEPTPSPQAR  
 KGLHPNPTVRDLVSVDSDSRSTESTPAGSETKDIRL"

BASE COUNT 517 a 737 c 705 g 582 t 1 others

NRGIN

Query Match 9.3%; Score 100.4; DB 11; Length 2542;  
 Best Local Similarity 51.3%; Pred. No. 2e-17;  
 Matches 233; Conservative 0; Mismatches 221; Indels 0; Gaps 0;

160 TCCCTTTATTTATGATATCTCTCGTGGATTTCCAGGAAAGCACTGATATAT 219  
 590 TCGCCGTCCTATGCGTGTGCTGCGGTGTGCTGAAGCTGCTGCTCT 649  
 220 CCACTTACATTTCAAAAGAGACCTTTGGAAGAGACACCATATATGCTGAACCTG 279  
 650 ATATCTTCTTATCCGCTCAAAACCTGGAACGCTCCACCACTACATGTTTACCTGG 709  
 280 CCTGCACAGATCTGCTATCTGACAGCCCTCCCTCTGATTCACATCAGTACAGT 339  
 710 CAGTTTGGAGCTCTCTGAGCAGCGCCCTGCGCTGTTGTTTATTAACCCCGGG 769  
 340 GCGAAAGTGAATCTTTGAGATTAATGATTAATCGCTTACAGTCCATTTCA 399  
 770 GTGACACATGGCCATTTAGACAGGTGCTGCAAGCTGAGCGGTTTCTCTTCAACCA 829  
 400 ACCGTATAGCAGCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 459  
 830 ACCCTTACAGCAGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 889  
 460 TTCACCCATGAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 519  
 890 TCGGCTCTGACCTCCCGCGTGGGCGCGCGCTTTATGCGCGCGGAGTGGCTGG 949  
 520 TGGTGTGATCAATTTCACTGTGATGCTGATTCGATGACCTTCTTATGATCAATCA 579  
 950 TTGTGTGGGTGCTGTGCTGCTGCGGACGACCGCTGCTTACTGATCAACACAGCG 1009

cy 580 ACAGGACCAACAGATCAGCTGTCTGACCTCAC 613  
 db 1010 TCGCGGAAACCGGATCACTTCCATGACACCTC 1043

RESULT 12  
 AK005013  
 LOCUS  
 DEFINITION  
 Mus musculus adult male liver cDNA, RIKEN full-length enriched library, clone:1300015C04; putative receptor P2Y, G-protein coupled 2, full insert sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 AK005013  
 AK005013  
 AK005013  
 GI:12836638  
 HTC; CAP trapper.  
 Mus musculus (strain: C57BL/6J) adult male liver cDNA to mRNA, clone:1300015C04.  
 Mus musculus  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## ORGANISM

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 1 Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning  
 Meth. Enzymol. 303, 19-44 (1999)  
 99279253  
 10349636  
 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
 Genome Res. 10 (10), 1617-1630 (2000)  
 20499374  
 11042159  
 3

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 1 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komno, H., Akiyama, J., Nishi, K., Kikunishi, T., Tashiro, H., Itoh, M., Sumi, M., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
 Genome Res. 10 (11), 1757-1771 (2000)  
 20530913  
 11076861  
 4

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 1 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, T., Hara, A., Fukunishi, Y., Komno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamataka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsumura, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, F., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Niki, C., Pesole, G., Quackenbush, J., Schriml, L. M., Staudli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Balderelli, R., Barsch, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombauts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schombach, C., Seta, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S., and Hayashizaki, Y.  
 Functional annotation of a full-length mouse cDNA collection  
 Nature 409 (6821), 685-690 (2001)  
 21085660  
 11217851  
 5 (bases 1 to 3001)  
 Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A.,



BASE COUNT 83 a 163 c 125 g 108 t 12 others  
 RIGIN

Query Match 9.8%; Score 106.2; DB 12; Length 491;  
 Best Local Similarity 59.4%; Pred. No. 2.1e-19;  
 Matches 168; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

145 TCAAGATGCACTACCTCCCTGTTATTTATTTAGCATTTATCTCTGCGGATTTCCAGGCA 204  
 209 TCAAGTTCATCTCCGCTGCTCCATCTCCACGCGCATCTCTGCTGCGGATTTCCAGGCA 268  
 205 ATGCAATGATGATTCACATTTTCAATTTGAGACCTTTGGAAGAGACGACCATCA 264  
 269 ACTCTGGGCGCATGTGATTTTGTCTCCAGAGTAGGCGCTTGAGACGCGACCATCACTT 328  
 265 TTATGCTGAACCTGCGCTGACAGATCTGTATCTGACAGCGCTCCCTCTCTGATTC 324  
 329 ACATGTTTAACTTACAGCATCTGACAGCGCTCTATGCTCTCTCCCTCCACCTGATCT 388  
 325 ACTACTATGCGCAGTGGCGAAACTGATCTTTTGAGATTTTCATGTGATTTATCCGCT 384  
 389 ACTACTACCTGACCGCCCAACACTGCGCTCCNNGGAAGTGTGTGNNNNNNNNCGCT 448  
 385 TCAGCTTCCATTTCACTCTGTATGACGACATCTCTCTCCAC 427  
 449 TTTCTCTTACCGCCCACTCTACAGCAGCATCTCTCTCTGAC 491

RESULT 9  
 LOCUS AL588350 609 bp mRNA linear EST 02-MAY-2001  
 DEFINITION AL588350 BP Chicken Brain Library Gallus gallus cDNA clone  
 ROS071B08, mRNA sequence.

ACCESSION AL588350  
 VERSION AL588350.1 GI:13193384  
 KEYWORDS EST.

ORGANISM Gallus gallus  
 SOURCE chicken.

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 609)

AUTHORS Murray, F.  
 TITLE BP Chicken Brain Library  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Frazer Murray  
 Dept. Genomics and Bioinformatics  
 Roslin Institute  
 Roslin, Midlothian, EH25 9PS, UK  
 Tel: +44 (0)131 527 4200  
 Fax: +44 (0)131 440 0434  
 Email: frazer.murray@rosc.ac.uk  
 GCGGCGGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech  
 (\*6854-  
 Seq primer: T7.

FEATURES  
 source

Location/Qualifiers  
 1..609  
 /organism="Gallus gallus"  
 /db\_xref="taxon:9031"  
 /clone\_lib="ROS071B08"  
 /clone\_lib="BP Chicken Brain Library"  
 /issue\_type="Brain"  
 /dev\_stage="Unknown"  
 /lab\_host="DH10B"  
 /note="Vector: pSPORT1, Site 1: NotI, Site 2: SalI; Cloned  
 unidirectionally. Primer: Oligo dt. 5' adaptor sequence:  
 5' TCACTCGAG 3' ; 3' adaptor sequence: 5'  
 GCGGCGGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from  
 Clontech (\*6854-1)"

BASE COUNT 101 a 199 c 189 g 117 t 3 others  
 RIGIN

Query Match 9.5%; Score 103; DB 9; Length 609;  
 Best Local Similarity 59.1%; Pred. No. 1.9e-18;  
 Matches 175; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

145 TCAAGATGCACTACCTCCCTGTTATTTATTTAGCATTTATCTCTGCGGATTTCCAGGCA 204  
 293 TCAAGTTCATCTCCGCTGCTCCATCTCCACGCGCATCTCTGCTGCGGATTTCCAGGCA 352  
 205 ATGCAATGATGATTCACATTTTCAATTTGAGACCTTTGGAAGAGACGACCATCA 264  
 353 ACAGCGGCGCATGTGATTTGCTTCCACATGCGCGGTGAGGCGCATCTCGGCT 412  
 265 TTATGCTGAACCTGCGCTGACAGATCTGTATCTGACAGCGCTCCCTCTCTGATTC 324  
 413 ACATGTTTAACTTACAGCATCTGACAGCGCTCTATGCTCTCTCCCTCCACCTGATCT 472  
 325 ACTACTATGCGCAGTGGCGAAACTGATCTTTTGAGATTTTCATGTGATTTATCCGCT 384  
 473 TCACTACTTCAACAAACGATCTGATCTTCCGCGGACGTCATGTGACAGCTGACAGGT 532  
 385 TCAGCTTCCATTTCACTCTGTATGACGACATCTCTCTCCACCTGTTTACAGATC 440  
 533 TCAATTTCCAGTGAACCTCTACGCGCAGCATCTGTTTCTCACGTCATTAAGCGTC 588

RESULT 10  
 LOCUS A1663305 520 bp mRNA linear EST 10-MAY-1999  
 DEFINITION uk27c10.y1 Sugano mouse kidney mKia Mus musculus cDNA clone  
 IMAGE:1970226.5, similar to SW:P2YR\_PAT P49651 P2Y PURINOCPTOR 1  
 mRNA sequence.

ACCESSION A1663305  
 VERSION A1663305.1 GI:4766888  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 520)  
 AUTHORS Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wyllie, T.,  
 Underwood, K., Stepfede, M., Theising, B., Allen, M., Bowers, Y., Person  
 B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Rittler  
 E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,  
 Waterston, R., and Wilson, R.  
 The WashU-NCI Mouse EST Project 1999  
 Unpublished (1999)  
 Other ESTs: uk27c10.x1

TITLE Contact: Marra M/WashU-NCI Mouse EST Project 1999  
 JOURNAL Washington University School of Medicine  
 COMMENT 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LML; contact the  
 IMAG Consortium (info@image.lml.gov) for further information.  
 MGI:986966  
 Seq primer: custom primer used  
 High quality sequence stop: 490.

FEATURES  
 source

Location/Qualifiers  
 1..520  
 /organism="Mus musculus"  
 /strain="C57BL"  
 /db\_xref="taxon:10090"  
 /clone\_lib="IMAGE:1970226"  
 /clone\_lib="Sugano mouse kidney mKia"  
 /sex="Female"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"

/note="Organ: kidney; Vector: pMR188-Flu3; Site 1: DraIII  
 (CACTGATG); Site 2: DraIII (CAACATGG); 1st strand cDNA  
 was primed with an oligo(dT) primer  
 (ATGTGCGCTTTTCTTTTCTTTT) ; double-stranded cDNA was  
 ligated to a DraIII adaptor (TGTGGCGCTTACG3), digested

Db	Accession	Version	Keywords	Source	Organism	Reference	Authors	Title	Journal	Comment
Db	421	GCCTCCCTGGGATGTGCTACCCATGAAATCACTCGGTGGCTGGAAGTGGGAATGCTC	480							
Qy	505	TTGTAGCCTGTGCTGTGCTGTGATCATTTTCATGTAGCTGTTCATCCGATGACCTTCT	564							
Db	481	GGATTAATTTCCGTGTGCTGTGGTTATCGTTTCGCCGCTCAGTCCCTTAATATTTGACT	540							
Qy	565	TGATCATATCAACCAAGACCAAGATGATGAGCTGTCTGCACCTTCACGATTTGGATG	624							
Db	541	TTGTATACCACTGTTCCATATGGGACGACCACTGTCATGACACTTTCAGCGGTGATC	600							
Qy	625	AACTAATATATTAATGATGATACAC	650							
Db	601	TATTTGACACTTGTGTGCTTACAGC	626							
RESULT 5	BG402029	877 bp	mRNA	linear	EST 12-MAR-2001					
LOCUS	602466748F1 NIH_MGC_75	Homo sapiens	CDNA clone	IMAGE:4594810 5',						
DEFINITION	mRNA sequence.									
ACCESSION	BG402029									
VERSION	BG402029.1	GI:13295477								
KEYWORDS	EST.									
SOURCE	human.									
ORGANISM	Homo sapiens									
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.									
TITLE	NIH-MGC http://mgc.nci.nih.gov/.									
JOURNAL	1 (bases 1 to 877)									
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)									
	Unpublished (1999)									
	Contact: Robert Strausberg, Ph.D.									
	Email: cgapbs-remail.nih.gov									
	Tissue Procurement: CLONTECH Laboratories, Inc.									
	CDNA Library Preparation: CLONTECH Laboratories, Inc.									
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)									
	DNA Sequencing by: Incyte Genomics, Inc.									
	Clone distribution: MGC clone distribution information can be									
	found through the I.M.A.G.E. Consortium/LMNL at:									
	http://lmnl.llnl.gov									
	Plate: L1CM1336 row: p column: 11									
	High quality sequence stop: 542.									
FEATURES	Location/Qualifiers									
Source	1..877									
	/Organism="Homo sapiens"									
	/db_xref="taxon:9606"									
	/clone="IMAGE:4594810"									
	/clone_lib="NIH_MGC_75"									
	/lab_host="DH10B (TI phage-resistant)"									
	/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:									
	SfiI (ggcgccgcgcgcgc); Site 2: SfiI (ggcgccatctggcc); 5' and									
	3' adaptors were used in cloning as follows: 5' adaptor									
	sequence: 5'-CAGCGCCATTAATGAC-3' and 3' adaptor sequence:									
	5'-ATTCTAGAGGCCGAGCGCCGACATG-dt(30)BN-3' (where B = A,									
	C, or G and N = A, C, G, or T). Average insert size 1.65									
	kb (range 0.5-4.0 kb). 15/15 colonies contained inserts									
	by PCR. This library was enriched for full-length clones									
	and was constructed by Clontech Laboratories (Palo Alto,									
	CA). Note: this is a NIH_MGC Library."									
BASE COUNT	198 a 221 c 199 g 259 t									

Db	185	TTTTATGGGATTGAGTTCCTGTGTGGGAGTCTTGGAAATACCATTTGTTTACGGCTAC	244			
Qy	228	ATTTCACAAATAGACCTTTGGAAGACGACACCATCATTTATGCTGAACTGGCTGCACA	287			
Db	245	ATCTCTCTCTGAAGAACTGAAACAGCAGTAAATATTATCTTTAACTCTCTGTCTCT	304			
Qy	288	GATTCGCTGTACTGACCGACCTCCCTCTTCCGATTCACACTATGACGAGTGGCGAAAC	347			
Db	305	GACTTAGCTTTTCTGTGACCCCTCCCAATGCTGGAATAGGATTAAGCCATGG---AAAC	361			
Qy	348	TGGATCTTTGGAGATTTCATGTGTAAAGTTTATCCGCTTCAGCTTCACATTTCAACCTGAT	407			
Db	362	TGGATTAATAGGAGAGTGTGTCTGCATTAAGCAACCATATGTGCTTACGACCACTCTAT	421			
Qy	408	AGACGATCTCTTCTTCTCACTGTTTTCAGCATCTTCCGCTACTGTGTATCATTCACCC	466			
Db	422	ACCAGCATCTCTTCTCACTTTCATTCAGCATATGATTCGATTCGATTAATTAAGTATCC	480			
RESULT 5						
BM426517						
LOCUS	663 bp	mRNA	linear			
DEFINITION	pgf2n.pk002.06 Normalized Chicken Abdominal Fat Library (pgf2n)					
Gallus gallus cDNA clone pf2n.pk002.06 5' similar to						
sp P34996 P2YR.CHICK P2Y PURINORECEPTOR 1 (ATP RECEPTOR) (P2Y1)						
(PURINERGIC RECEPTOR) p1r1533733 G protein-coupled receptor -						
chicken emb CMA51716.1  (X73268) ATP receptor P2Y1 [Gallus gallus],						
mRNA sequence.						
BM426517						
ACCESSION	BM426517.1					
VERSION	GI:18430913					
KEYWORDS	EST.					
SOURCE	chicken.					
ORGANISM	Gallus gallus					
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;						
Phasianinae; Gallus.						
1 (bases 1 to 663)						
REFERENCE	Coggburn, L.A., Morgan, R. and Burnside, J.					
AUTHORS	ESTs from Normalized Chicken fat cDNA library-USDA/IFARS Animal					
TITLE	Genome Project					
JOURNAL	Unpublished (2002)					
COMMENT	Contact: Larry A. Coggburn					
University of Delaware						
Townsend Hall, Newark, DE 19717, USA						
Tel: 302-831-1335						
Fax: 302-831-2822						
Email: coggburn@udel.edu, www.chickest.udel.edu.						
FEATURES	Location/Qualifiers					
SOURCE	1..663					
/organism="Gallus gallus"						
/strain="Commercial broiler, Ottawa Research Centre,						
leghorn"						
/db xref="taxon:9031"						
/clone="pgf2n.pk002.06"						
/clone_lib="Normalized Chicken Abdominal Fat Library						
(pgf2n)"						
/sex="Male and Female"						
/tissue_type="Abdominal Fat"						
/dev stage="Embryonic (d18,d19); post-hatch (d1,w3,w7,w9						
w16,1yr)"						
/lab_host="E. coli EMDH10B"						
/note="Vector: PCMVSPORT6; Library made from equivalent						
pools of total RNA isolated from each developmental age						
(across strains); Single pass sequencing from 5'-end"						
BASE COUNT	102 a	223 c	210 g			
ORIGIN	121 t	7 others				
Query Match						
Best Local Similarity 57.5%; Pred. No. 4.2e-20;						
Matches 189; Conservative 0; Mismatches 139; Indels 0; Gaps 0;						
145	TCAAGATGACATACCTCCGTGTAATTATGAGCATTAATCTTCTCGTGGAGATTTCAGGCA					
204						

Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).  
Seq primer: M13 Reverse.  
Location/Qualifiers

1. 744

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="UI-E-BO1-aiX-9-16-0-UI"

/clone\_lib="UI-E-BO1"

/tissue\_type="fetal eye"

/dev\_stage="fetal"

/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"

/note="Organ: eye; Vector: pRTT3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-BO1 is a normalized cDNA library containing the following tissue(s): fetal eye. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pRTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GCGGTATAC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

BASE COUNT 217 a 168 c 126 g 233 t

ORIGIN

Query Match 23.8%; Score 257; DB 14; Length 744;  
Best Local Similarity 100.0%; Pred. No. 8.4e-63;  
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

825 CATATCTGAGGGTCAATTCGATCGAATCTCGCTCTTCATCATGTTGTCATTGAG 884  
b 1 CATATCTGAGGGTCAATTCGATCGAATCTCGCTCTTCATCATGTTGTCATTGAG 60  
Y 885 AATCGATCCATGAAGCTTACATCGTTTTCAGACCATTAAGCTCTGAAACACCTTGGT 944  
b 61 AATCGATCCATGAAGCTTACATCGTTTTCAGACCATTAAGCTCTGAAACACCTTGGT 120  
Y 945 AACCGTACTATATGTTGTTGTCAGCGCACTTTCAGACGAGCTGTCTGTAACAGTG 1004  
b 121 AACCTGTACTATATGTTGTTGTCAGCGCACTTTCAGACGAGCTGTCTGTAACAGTG 180  
Y 1005 AGATGCAAGTAAAGGGAACCTTGAGCAAGCAAGAAATTGTTACTCAACAACCTT 1064  
b 181 AGATGCAAGTAAAGGGAACCTTGAGCAAGCAAGAAATTGTTACTCAACAACCTT 240  
Y 1065 TGAATATTTTCATTAC 1081  
b 241 TGAATATTTTCATTAC 257

ESULT 2 623 bp mRNA linear EST 01-MAY-2002  
2018875

DEFINITION B0038875 623 bp mRNA linear EST 01-MAY-2002  
gnic.pk010.113 normalized chicken lymphoid cDNA library Gallus  
gallus cDNA clone gnic.pk010.113 5' similar to  
sp|P34996|P2YR\_CHICK\_P2Y\_PURINORECEPTOR\_1 (ATP RECEPTOR) (P2Y1)  
(PURINERGIC RECEPTOR) p1r|S33733 G protein-coupled receptor -  
chicken emb|CMA51716.1| (X73268) ATP receptor P2Y1 [Gallus gallus],  
mRNA sequence.

ACCESSION B0038875  
VERSION B0038875.2 GI:20383637

ORIGIN B0038875.2 GI:20383637

ORIGIN B0038875.2 GI:20383637

ORGANISM Gallus gallus  
chicken.  
Archaeopteryx; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Rukhsauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 623)  
AUTHORS Morgan, R.W. and Burnside, J.  
TITLE Chicken lymphoid ESTs  
JOURNAL Unpublished (2001)  
COMMENT On Mar 27, 2002 this sequence version replaced gi:19772415.  
Contact: Joan Burnside  
Molecular Endocrinology  
University of Delaware  
40 Townsend Hall, Newark, DE 19717, USA  
Tel: 302 831-1345  
Fax: 302-831-3411  
Email: joan@udel.edu, www.chickest.udel.edu.

FEATURES  
Source location/Qualifiers

1. 623

/organism="Gallus gallus"

/db\_xref="taxon:9031"

/clone="gnic.pk010.113"

/clone\_lib="normalized chicken lymphoid cDNA library"

/sex="Male and Female"

/tissue\_type="thymus, bursa, spleen, PBL, bone marrow"

/lab\_host="E.coli EMDH10B"

/note="Vector: PCWVSPORT 6"

BASE COUNT 117 a 199 c 172 g 128 t 7 others

ORIGIN

Query Match 11.7%; Score 126.6; DB 14; Length 623;  
Best Local Similarity 53.6%; Pred. No. 3e-25;  
Matches 258; Conservative 0; Mismatches 223; Indels 0; Gaps 0;

145 TCAAGATGACATACCTCTCTGTTATTTAGGCAATATCTCTCTGTTGAGGCA 204  
Db 124 TCCAGTTCTACTACCTGACCCGCTACATCTCTCTCTCTCTCTCTCTCTCTCT 183  
Y 205 ATCAGATGATATTCATCTTACATTTTCAATATGAGACCTTGAAGAGACATCA 264  
Db 184 ACAGCTGGCATCTGATGTTGTTCTTCAATGCGCGCTGAGCGGATCTGGTGT 243  
Y 265 TTAAGCTGAACCTGCTGACAGATCTGCTGATCTGACAGCTCTCCCTCTGATTC 324  
Db 244 ACATGTTCAACCTGCTGCGGCGGACTTCTGATCTCTGACGCTGCGGCTCTATCT 303  
Y 325 ACTACTATGACGAGGCGGAAACCTGATCTTGGAGATTTGATGTTATTCGCT 384  
Db 304 TCTACTACTTCAACAAACGACCTGATCTTGGGAGACGTCATGTCAGCTCAGAGGT 363  
Y 385 TCAAGCTTCAATTTCAACCTGATGAGCATCTCTCTCTCTCTCTCTCTCTCTCT 444  
Db 364 TCAATTTCAACGAGGACCTTACGCGGACATCTCTCTCTCTCTCTCTCTCTCTCT 423  
Y 445 GCTACTGTGATCAATTCACCAATGAGCTGTTTCCATTCAAAATCGATGTGAG 504  
Db 424 GGTACAGGCGGCTCTGACCCGCTGAAATGCTGAGGAGGCTGAAGAAAGAACGCG 483  
Y 505 TTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 564  
Db 484 TGTAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 543  
Y 565 TCAATCAATCAACCAAGACCAACAGATCAAGCTGCTGCTGCTGCTGCTGCTGCTG 624  
Db 544 ACTCAGGAGCGGNNNGTGGAGGAGCAAAACCATCATCGTTCACGACGAGGAGAG 603  
Y 625 A 625  
Db 604 A 604

RESULT 3

LOCUS B0396255

DEFINITION B0396255 641 bp mRNA linear EST 22-MAY-2002

ACCESSION B0396255

VERSION B0396255.1 GI:21083932

gnic.pk010.113 normalized chicken lymphoid cDNA library Gallus  
gallus cDNA clone gnic.pk010.113 5' similar to  
sp|P34996|P2YR\_CHICK\_P2Y\_PURINORECEPTOR\_1 (ATP RECEPTOR) (P2Y1)  
(PURINERGIC RECEPTOR) p1r|S33733 G protein-coupled receptor -  
chicken emb|CMA51716.1| (X73268) ATP receptor P2Y1 [Gallus gallus],  
mRNA sequence.

```

|||||
b 1 ATGATGAGCCACTGAGCTATTATAGCAAAAGCTTCTGATTTCCCGATTATGACGCTCT 60
y 114 TTGGAAATTCACATGATGAAACATCCCACTCAAGATGACACTACCTCCCTGTTATTAT 173
b 61 TTGGAAATTCACATGATGAAACATCCCACTCAAGATGACACTACCTCCCTGTTATTAT 120
y 174 GGCATTTATCTCTCTGTTGGGATTTCCAGGCAATGCACTGATGATATCCACTTACATTTTC 233
b 121 GGCATTTATCTCTCTGTTGGGATTTCCAGGCAATGCACTGATGATATCCACTTACATTTTC 180
y 234 AAATGAGACCTTGGAAGAGGAGCAACCATATTATGCTGACCTGGGCTGACAGATCTG 293
b 181 AAATGAGACCTTGGAAGAGGAGCAACCATATTATGCTGACCTGGGCTGACAGATCTG 240
y 294 CTGTATCTGACGAGCTCCCTCTCTGATTTCACTATGCAAGTGGGCAAACTGATC 353
b 241 CTGTATCTGACGAGCTCCCTCTCTGATTTCACTATGCAAGTGGGCAAACTGATC 300
y 354 TTGGAGATTTGATGTTGATGTTATCCGCTTCAAGCTTCACTTTCACTGTTATGACGC 413
b 301 TTGGAGATTTGATGTTGATGTTATCCGCTTCAAGCTTCACTTTCACTGTTATGACGC 360
y 414 ATCCCTCTCCCTGACCTGTTTCAAGCATCTCCGCTACTGATGATCATTCACCAATGAGC 473
b 361 ATCCCTCTCCCTGACCTGTTTCAAGCATCTCCGCTACTGATGATCATTCACCAATGAGC 420
y 474 TGCCTTTCATTCACAAACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 533
b 421 TGCCTTTCATTCACAAACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
y 534 TCACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 593
b 481 TCACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
y 594 TCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 653
b 541 TCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
y 654 ATTTGACTGCAACTCTTCTGCTCCCTGCTGATGATGATGATGATGATGATGATGATGAT 713
b 601 ATTTGACTGCAACTCTTCTGCTCCCTGCTGATGATGATGATGATGATGATGATGATGAT 660
y 714 ATTATCCACACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCA 773
b 661 ATTATCCACACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCA 720
y 774 AGGCTAACCATTTCTGCTACTCCCTGCACTTTAGTATGTTTAACTCCCTCAATCTTG 833
b 721 AGGCTAACCATTTCTGCTACTCCCTGCACTTTAGTATGTTTAACTCCCTCAATCTTG 780
y 834 AGGCTAACCATTTCTGCTACTCCCTGCACTTTAGTATGTTTAACTCCCTCAATCTTG 893
b 781 AGGCTAACCATTTCTGCTACTCCCTGCACTTTAGTATGTTTAACTCCCTCAATCTTG 840
y 894 CATGAAGCTTACATCGTTTCTAGACCATTAAGCTGCTGTAACACCTTGTAACTGTTA 953
b 841 CATGAAGCTTACATCGTTTCTAGACCATTAAGCTGCTGTAACACCTTGTAACTGTTA 900
y 954 CTATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1013
b 901 CTATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 960
y 1014 GTTAAAGGGGAGCTTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCTTGA 1067
b 961 GTTAAAGGGGAGCTTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCTTGA 1014

```

QY 174 GGCATTATCTTCTCGTGGGATTTTCAGGCAATGACAGTAGTATATCCATTACATTTTC 233  
 DB 121 GGCATTATCTTCTCGTGGGATTTTCAGGCAATGACAGTAGTATATCCATTACATTTTC 180  
 QY 234 AAAATGAGACCTTGGAGAGACGACACATCATTTATGCTGAACCTGGCTGCACAGATCTG 293  
 DB 181 AAAATGAGACCTTGGAGAGAGACGACACATCATTTATGCTGAACCTGGCTGCACAGATCTG 240  
 QY 294 CTGATCTGACAGGCTCCCTTCTGATTCATCTATAGCCAGTGGCCAAAACCTGGATC 353  
 DB 241 CTGATCTGACAGGCTCCCTTCTGATTCATCTATAGCCAGTGGCCAAAACCTGGATC 300  
 QY 354 TTTGAGATTTGATGATGATTTATCCGCTTCAAGCTTCATTTCAACCTGATAGACG 413  
 DB 301 TTTGAGATTTGATGATGATTTATCCGCTTCAAGCTTCATTTCAACCTGATAGACG 360  
 QY 414 ATCTCTTCTCTCAGCTGTTTTCAGCATCTTCCGCTACTGTGTATCATTCACCCATGAGC 473  
 DB 361 ATCTCTTCTCTCAGCTGTTTTCAGCATCTTCCGCTACTGTGTATCATTCACCCATGAGC 420  
 QY 474 TGCCTTTTCATTCACAAAACCTGATGTGAGTTGAGCTGTGCTGTGTGTGATCATTT 533  
 DB 421 TGCCTTTTCATTCACAAAACCTGATGTGAGTTGAGCTGTGCTGTGTGTGATCATTT 480  
 QY 534 TCACCTGTAGCTGTGATTCGAGTACCTTCTGATCATCATCAACCAAGGACCAACAG 593  
 DB 481 TCACCTGTAGCTGTGATTCGAGTACCTTCTGATCATCATCAACCAAGGACCAACAG 540  
 QY 594 TCAGCTGTCTGACCTTCACAGCTTGCAGTGAAGTCAATCTATTAAAGTGTCAACCTG 653  
 DB 541 TCAGCTGTCTGACCTTCACAGCTTGCAGTGAAGTCAATCTATTAAAGTGTCAACCTG 600  
 QY 654 ATTTGACTGCACTACTTCTTGTGCTCCCTTGTGTATGATGACACTTGTGTATACCAAG 713  
 DB 601 ATTTGACTGCACTACTTCTTGTGCTCCCTTGTGTATGATGACACTTGTGTATACCAAG 660  
 QY 714 ATTATCCACACTCTGACCCGATGAGTGAAGTCAACGAGCTGCTTAAAGGAGAAAGCA 773  
 DB 661 ATTATCCACACTCTGACCCGATGAGTGAAGTCAACGAGCTGCTTAAAGGAGAAAGCA 720  
 QY 774 AGGCTAACCATCTCTGCTACTCTCTTGCATTTTACGATGTTTAACTTCCATATCTTG 833  
 DB 721 AGGCTAACCATCTCTGCTACTCTCTTGCATTTTACGATGTTTAACTTCCATATCTTG 780  
 QY 834 AGGCTATTCGGATGATCTGCTGCTCTTCAATGATGTTTCCATGGAATGCAATC 893  
 DB 781 AGGCTATTCGGATGATCTGCTGCTCTTCAATGATGTTTCCATGGAATGCAATC 840  
 QY 894 CATGAGCTTATATGCTTCTAGACCATTAAGCTGCTTGAACACCTTGTATCCTGTTA 953  
 DB 841 CATGAGCTTATATGCTTCTAGACCATTAAGCTGCTTGAACACCTTGTATCCTGTTA 900  
 QY 954 CTATATGTGTGTGTGTCAGGACAACTTTCAGCAGGCTGTCTCAACAGTGAATGCAAA 1013  
 DB 901 CTATATGTGTGTGTGTCAGGACAACTTTCAGCAGGCTGTCTCAACAGTGAATGCAAA 960  
 QY 1014 GTAAACGGGAACTTGGAGCAAGCAAAAGAAATTTAGTTACTCAAAACACCTTGA 1067  
 DB 961 GTAAACGGGAACTTGGAGCAAGCAAAAGAAATTTAGTTACTCAAAACACCTTGA 1014  
 RESULT 14  
 AAD34278 standard; cDNA; 1014 BP.  
 ID AAD34278  
 AC AAD34278;  
 XX AAD34278;  
 DT 16-JUN-2002 (first entry)  
 DE Human AXOR89 (G-protein coupled receptor) cDNA.  
 XX Human AXOR89 polypeptide; G-protein coupled receptor; vaccine; receptor;  
 KW Human; AXOR89 polypeptide; G-protein coupled receptor; vaccine; receptor;  
 infection; cancer; pain; asthma; Parkinson's Disease; diabetes; obesity;

KW anorexia; bulimia; acute heart failure; hypotension; hypertension; ulcer;  
 KW stroke; urinary retention; osteoporosis; angina pectoris; schizophrenia;  
 KW myocardial infarction; allergy; benign prostatic hypertrophy; migraine;  
 KW vomiting; psychotic; neurological disorder; anxiety; manic depression;  
 KW delirium; Huntington's Disease; Gilles de la Tourette's syndrome;  
 KW dementia; dyskinesia; gene; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 1..1014  
 FT /tag= a'  
 FT /product= "Human AXOR89 protein"  
 PN GB2365012-A.  
 PD 13-FEB-2002.  
 PD 10-MAY-2001; 2001GB-0011437.  
 PF 11-MAY-2000; 2000US-0569137.  
 PR (SMK) SMITHKLINE BEECHAM CORP.  
 PA (SMK) SMITHKLINE BEECHAM PLC.  
 PI Elshourbagy N, Shabon U;  
 DR WPI; 2002-332558/37.  
 DR P-PSDB; AAE21803.  
 PT Novel AXOR89 polypeptide and polynucleotide encoding it, useful for  
 PT identifying agonists and antagonists in the treatment of diseases  
 PT associated with an AXOR89 imbalance, such as cancers, diabetes or  
 PT asthma.  
 PS Claim 2; Page 30; 37pp; English.  
 XX The invention relates to an isolated AXOR89 polypeptide (G-protein  
 CC coupled receptor) and its polynucleotide. The novel AXOR89 polypeptide  
 CC and polynucleotide encoding the polypeptide, is useful for identifying  
 CC agonists and antagonists (or inhibitors) that are potentially useful in  
 CC treating conditions associated with an AXOR89 imbalance, such as  
 CC bacterial, fungal or protozoan infections, cancers, pain, asthma,  
 CC Parkinson's Disease, diabetes, obesity, anorexia, bulimia, acute heart  
 CC failure, hypotension, hypertension, urinary retention, osteoporosis,  
 CC angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign  
 CC prostatic hypertrophy, migraine, vomiting, psychotic and neurological  
 CC disorders, anxiety, schizophrenia, manic depression, delirium, dementia,  
 CC dyskinesias, such as Huntington's Disease or Gilles de la Tourette's  
 CC syndrome. The polynucleotide sequence may also be used for chromosome  
 CC localisation or tissue expression studies. The AXOR89 is used as a  
 CC vaccine or to produce fusion proteins. The present sequence is human  
 CC AXOR89 cDNA.  
 XX  
 SQ Sequence 1014 BP; 259 A; 263 C; 188 G; 304 T; 0 other;  
 Query Match 93.7%; Score 1012.4; DB 24; Length 1014;  
 Best Local Similarity 99.9%; Pred. No. 8.5e-287;  
 Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 54 ATGAATGAGCCACTAGACTATTTAGCAAAATGCTTGTGATTTCCCGGATTTAGCAGCTGCT 113  
 DB 1 ATGAATGAGCCACTAGACTATTTAGCAAAATGCTTGTGATTTCCCGGATTTAGCAGCTGCT 60  
 QY 114 TTTGAAATTTGACCTGATGAAAAATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 173  
 DB 61 TTTGAAATTTGACCTGATGAAAAATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120  
 QY 174 GGCATTATCTTCTCGTGGGATTTTCAGGCAATGACAGTAGTATATCCATTACATTTTC 233  
 DB 121 GGCATTATCTTCTCGTGGGATTTTCAGGCAATGACAGTAGTATATCCATTACATTTTC 180  
 QY 234 AAAATGAGACCTTGGAGAGACGACACATCATTTATGCTGAACCTGGCTGCACAGATCTG 293

Severe mental retardation, Huntington's disease and Tourette's syndrome.  
The present sequence encodes the P2Y1-like GPCR of the invention.  
Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 other;

Query Match 93.8%; Score 1014; DB 24; Length 1014;  
Best Local Similarity 100.0%; Pred. No. 2.9e-287; Indels 0; Gaps 0;  
Matches 1014; Conservative 0; Mismatches 0;

54 ATGAATGAGGCACTAGACTATTAGCAAAATGCTCTGATTTCCCGATTTAGCAGTGT 113  
1 ATGAATGAGGCACTAGACTATTAGCAAAATGCTCTGATTTCCCGATTTAGCAGTGT 60  
114 TTGGAATTCGACGTAGTGAATCAATCCCACTCAAGATGACATACCTCTGTTATTTAT 173  
61 TTGGAATTCGACGTAGTGAATCAATCCCACTCAAGATGACATACCTCTGTTATTTAT 120  
174 GGCATTATCTTCTCGTGGGATTTCCAGGCAATGCAATGATGATATCACTTAATTTTC 233  
121 GGCATTATCTTCTCGTGGGATTTCCAGGCAATGCAATGATGATATCACTTAATTTTC 180  
234 AAAATGAGACCTTGAAGAGACAGACATATATGCTGAACCTGGCTGCAGATCTG 293  
181 AAAATGAGACCTTGAAGAGACAGACATATATGCTGAACCTGGCTGCAGATCTG 240  
294 CTGTATCTGACGACCTCCCTCTCTGATTCATCTATAGCAGTGGCGAAATGTGATC 353  
241 CTGTATCTGACGACCTCCCTCTCTGATTCATCTATAGCAGTGGCGAAATGTGATC 300  
354 TTGGAATTCGACGTAGTGAATCAATCCCACTCAAGATGACATACCTCTGTTATTTAT 413  
301 TTGGAATTCGACGTAGTGAATCAATCCCACTCAAGATGACATACCTCTGTTATTTAT 360  
414 ATCTCTCTCTGACCTGTTTGAAGATCTTCGCGTACGTGATATTCACCCATGAGC 473  
361 ATCTCTCTCTGACCTGTTTGAAGATCTTCGCGTACGTGATATTCACCCATGAGC 420  
474 TGCTTTCCATTCACAAACTCGATGTCAGTGTGATGCTGTGTGATCATTT 533  
421 TGCTTTCCATTCACAAACTCGATGTCAGTGTGATGCTGTGTGATCATTT 480  
534 TCACCTGAGTGTGATTCGATGTCAGTGTGATGTCAGTGTGATTCACCAACAGACAG 593  
481 TCACCTGAGTGTGATTCGATGTCAGTGTGATGTCAGTGTGATTCACCAACAGACAG 540  
594 TCACCTGAGTGTGATTCGATGTCAGTGTGATGTCAGTGTGATTCACCAACAGACAG 653  
541 TCACCTGAGTGTGATTCGATGTCAGTGTGATGTCAGTGTGATTCACCAACAGACAG 600  
654 ATTTGAGTGTGATTCGATGTCAGTGTGATGTCAGTGTGATTCACCAACAGACAG 713  
601 ATTTGAGTGTGATTCGATGTCAGTGTGATGTCAGTGTGATTCACCAACAGACAG 660  
714 ATTAATCCACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 773  
661 ATTAATCCACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 720  
774 AGGCTAACCAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 833  
721 AGGCTAACCAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
834 AGGCTAACCAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 893  
781 AGGCTAACCAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
894 CATGAAGCTTACATGCTTCTAGACCATATGCTGCTGAACACCTTGTGTAACCTGTTA 953  
841 CATGAAGCTTACATGCTTCTAGACCATATGCTGCTGAACACCTTGTGTAACCTGTTA 900  
954 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1013  
901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960

QY 1014 GTAAGGGGGAACCTTGAGCAAGCAAGAAATAGTACTCAACCAACCTTGA 1067  
DB 961 GTAAGGGGGAACCTTGAGCAAGCAAGAAATAGTACTCAACCAACCTTGA 1014

## RESULT 12

AAK98323  
ID AAK98323 standard; cDNA; 1014 BP.

AAK98323;  
30-APR-2002 (first entry)

XX  
AC  
XX  
XX  
DT  
XX

Human purinergic-related G-protein coupled receptor (GPCR) cDNA sequence.

XX Human; chromosome 13; purinergic GPCR; G-protein coupled receptor;  
XX signal transduction; human protease; GPCR disorder; gene therapy;  
KW transgenic animal; gene; ss.

XX Homo sapiens.

XX OS

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

Claim 23; Fig 1; 64pp; English.

The present specifically claimed human cDNA sequence (located on chromosome 13) encodes a purinergic-related G-protein coupled receptor (GPCR) of the invention. GPCRs constitute a major class of proteins responsible for signal transduction within a cell. Upon binding of a ligand to the extracellular portion of a GPCR, a signal is transduced resulting in a biological or physiological change within the cell. The GPCR proteins can be divided into five families, family I contains the purinergic GPCRs (e.g. the P2Y receptors). P2Y receptors are characterised by their selective responsiveness towards ATP and its analogues, some also respond to UTP. The invention comprises a human G-protein coupled receptor protein and encoding nucleic acids. The GPCR protein and nucleic acids of the invention are useful in the treatment of a disease or condition mediated by a human protease. The GPCR protein of the invention is useful for: the development/identification of therapeutic proteins; assays designed to quantitatively determine levels of the protein in biological fluids; identifying compounds which modulate the activity of the GPCR, or the interaction of the GPCR and a molecule with which it normally interacts; and treating a disorder characterised by an absence of, or inappropriate expression of the GPCR protein. The GPCR nucleic acids of the invention are useful in diagnostic assays to identify changes in the GPCR nucleic acid that lead to pathology; controlling GPCR expression; and in gene therapy to treat patients with aberrant GPCR gene expression. The GPCR nucleic acids can also be used in the production of transgenic animals.

cc The present sequence is that the P2Y<sub>1</sub>-like receptor variant encodes

CC immunosuppressive pain and general inflammation such as rheumatoid, CC  
CC polyostitis or prostaticitis. The invention provides alternative CC  
CC substances for the treatment of immunological and inflammatory diseases. CC  
CC The present sequence is that the P2Y-like receptor variant encoding gene





(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Schlegel R, Endege WO, Monahan JE;

WPI; 2001-662795/76.

Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -

Claim 1; Page 5175-5176; 11750pp; English.

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:  
 (a) assessing whether a patient is afflicted with prostate cancer;  
 (b) monitoring the progression of prostate cancer in a patient;  
 (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;  
 (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;  
 (e) selecting a composition for inhibiting prostate cancer in a patient;  
 (f) assessing the prostate cell carcinogenic potential of a compound;  
 (g) determining whether prostate cancer has metastasized in a patient;  
 (h) assessing the aggressiveness or indolence of prostate cancer in a patient;  
 (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

Sequence 1729 BP; 461 A; 401 C; 302 G; 548 T; 17 other;

Query Match 99.9%; Score 1079.4; DB 23; Length 1729;

Best Local Similarity 99.9%; Pred. No. 2.3e-306; Matches 1080; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 CATATTGCCAACTGAACTCTCTGTTTCTTGCAGATGAAAGAGACAACCATGAATG 60  
 241 CATATTGCCAACTGAACTCTCTGTTTCTTGCAGATGAAAGAGACAACCATGAATG 300  
 61 AGCCACTAGACTATTAGCAATAGCTTCTGATTTCCCGATTATGCACTGCTTTTGA 120  
 301 AGCCACTAGACTATTAGCAATAGCTTCTGATTTCCCGATTATGCACTGCTTTTGA 360  
 121 ATTGACATGATGAAACATCCCACTCAGATGCACTACCTCCCTGTTATTTATGGCATTA 180  
 361 ATTGACATGATGAAACATCCCACTCAGATGCACTACCTCCCTGTTATTTATGGCATTA 420  
 181 TCTTCTCTGCGAGATTCCAGCAATGAGATGATATCCACTTACATTTTCAAAATGA 240  
 421 TCTTCTCTGCGAGATTCCAGCAATGAGATGATATCCACTTACATTTTCAAAATGA 480  
 241 GACCTTGGAAAGAGAGACACATCATTTATGCTGAACCTGCGCTGACAGATCTGCTATC 300  
 481 GACCTTGGAAAGAGAGACACATCATTTATGCTGAACCTGCGCTGACAGATCTGCTATC 540  
 301 TGACCAACCTTCCCTCTCTGATTTCACTACTATGCGATGGGCAAAACATGATCTTTGAG 360  
 541 TGACCAACCTTCCCTCTCTGATTTCACTACTATGCGATGGGCAAAACATGATCTTTGAG 600  
 361 ATTTCATGTAAGTATTCGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCA 420  
 601 ATTTCATGTAAGTATTCGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCA 660  
 421 TCCCTACCTGTTTGAAGCATCTTCCGCTACTGTGTGATCATTCACCAATGAGCTCTTTT 480  
 661 TCCCTACCTGTTTGAAGCATCTTCCGCTACTGTGTGATCATTCACCAATGAGCTCTTTT 720  
 481 CCATTCAAAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540  
 721 CCATTCAAAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780  
 541 TAGCTGTCATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600  
 781 TAGCTGTCATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840

601 GTCTGACCTCACCAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATG 660  
 841 GTCTGACCTCACCAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATG 900  
 661 CTGCAACTACTTTCTGCTCTCCCTTGTGATGATGATGATGATGATGATGATGATGATG 720  
 901 CTGCAACTACTTTCTGCTCTCCCTTGTGATGATGATGATGATGATGATGATGATGATG 960  
 721 ACCTCTGACCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780  
 961 ACCTCTGACCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020  
 781 CCATTCTGCTACTCTGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 840  
 1021 CCATTCTGCTACTCTGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 1080  
 841 TTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900  
 1081 TTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140  
 901 CTTACATGTTTCTAGACATTAAGCTGCTGTAACACCTTTGTAACCTGTTACTATATG 960  
 1141 CTTACATGTTTCTAGACATTAAGCTGCTGTAACACCTTTGTAACCTGTTACTATATG 1200  
 961 TGTGTGTAGGAGCAACTTTGAGCAGGCTGTCTCAACAGTGAATGCAAGTAAGCG 1020  
 1201 TGTGTGTAGGAGCAACTTTGAGCAGGCTGTCTCAACAGTGAATGCAAGTAAGCG 1260  
 1021 GGAACCTTGACCAAGCAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1080  
 1261 GGAACCTTGACCAAGCAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1320  
 1081 C 1081  
 1321 C 1321

RESULT 6  
 ABV29909  
 ID ABV29909 standard; cDNA; 1729 BP.  
 XX AC  
 XX ABV29909;  
 XX AC  
 XX 16-SEP-2002 (first entry)  
 DT XX  
 XX Human prostate expression marker cDNA 2990.  
 DE XX  
 XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
 KW pharmacogenomic marker; gene; ss.  
 OS XX  
 OS Homo sapiens.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PD 23-AUG-2001.  
 PF 20-FEB-2001; 2001WO-US05171.  
 PR 17-FEB-2000; 2000US-183319P.  
 PR 16-MAR-2000; 2000US-189862P.  
 PR 25-MAY-2000; 2000US-207454P.  
 PR 09-JUN-2000; 2000US-211314P.  
 PR 18-JUL-2000; 2000US-219007P.  
 PR 13-DEC-2000; 2000US-255281P.  
 XX PA  
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 XX PI  
 XX Schlegel R, Endege WO, Monahan JE;  
 XX WPI; 2001-662795/76.  
 DR Novel isolated nucleic acid molecule associated with cancerous state of

XX 30-DEC-1999; 99US-0475790.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 PA Glucksmann MA, White D;  
 PI  
 XX MPI: 2001-432880/46.  
 DR P-PSDB; AAU04584.  
 PT Novel isolated 26904, 38911 and 39404 polypeptides which are seven  
 PT transmembrane proteins belonging to superfamily of G-protein-coupled  
 PT receptors, useful for treating disorders of spleen, lung, liver, brain  
 PT and kidney -  
 XX  
 PS Claim 2, Fig 1, 164pp; English.  
 XX The sequence encodes a novel human seven transmembrane domain  
 CC protein belonging to the G-protein coupled receptor (GPCR) superfamily,  
 CC protein 39404. The receptor is useful in drug screening assays, to  
 CC identify compounds that modulate receptor activity and/or interact with  
 CC the receptor, and for producing antibodies specific for the receptor, its  
 CC regions or fragments. The receptor is useful for treating/diagnosing a  
 CC 26904, 38911 and 39404 protein-associated disorder characterised by  
 CC aberrant expression or activity of the protein, for monitoring  
 CC therapeutic effect during clinical trials and other treatment, as bait  
 CC proteins in a two-hybrid or three-hybrid assay, and in pharmacogenomic  
 CC analysis. The proteins and nucleic acids encoding them are useful for  
 CC diagnosis and treatment of disorders selected from disorders of the  
 CC spleen, lung such as Good pasture's syndrome, liver such as viral  
 CC hepatitis, brain such as Alzheimer's disease, haematopoietic stem cells  
 CC such as lymphoma, kidney such as Heymann nephritis, bone such as Paget's  
 CC disease, colon such as Crohn's disease, uterus and endometrium such as  
 CC endometriosis, T-cell disorders such as systemic lupus erythematosus,  
 CC diseases of the skin such as acinic keratosis, disorders of the heart  
 CC such as myocarditis, disorders involving blood vessels such as Kawasaki  
 CC syndrome, disorders involving the thymus such as DiGeorge syndrome,  
 CC disorders involving B-cells such as peripheral B-cell neoplasms,  
 CC disorders of the breast such as inflammation, and disorders involving  
 CC the testis and epididymis such as teratoma. Numerous examples of  
 CC each type of disorder are given in the specification.  
 XX  
 30 Sequence 1729 BP; 461 A; 403 C; 302 G; 563 T; 0 other;  
 Query Match 99.9%; Score 1079.4; DB 22; Length 1729;  
 Best Local Similarity 99.9%; Pred. No. 2,3e-306;  
 Matches 1080; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 601 ATTTGATGTGTAAGTTTATCCGCTTCAAGCTTCATTGAACTGTATAGCAGATCTCTT 660  
 QY 421 TCCTCAGCTGTTTGAGCATCTTCGCTACTGTGTGATGATTCACCCAAATGAGCTGTTT 480  
 DB 661 TCCTCAGCTGTTTGAGCATCTTCGCTACTGTGTGATGATTCACCCAAATGAGCTGTTT 720  
 QY 481 CCATTCAAAAACCTGAGTGTGAGTTTGAAGCTGTGTGTGTGTGTGATCTTCACTG 540  
 DB 721 CCATTCAAAAACCTGAGTGTGAGTTTGAAGCTGTGTGTGTGTGTGATCTTCACTG 780  
 QY 541 TAGCTGTATTCGAGTGTGAGTTTGAAGCTGTGTGTGTGTGTGATCTTCACTG 600  
 DB 781 TAGCTGTATTCGAGTGTGAGTTTGAAGCTGTGTGTGTGTGTGATCTTCACTG 840  
 QY 601 GTCTGACCTGACCAAGTGTGTGAGTTTGAAGCTGTGTGTGTGTGATCTTCACTG 660  
 DB 841 GTCTGACCTGACCAAGTGTGTGAGTTTGAAGCTGTGTGTGTGTGATCTTCACTG 900  
 QY 661 CTGCAACTACTTCTGCTCCCTGTGTGTGTGTGTGATGACACTTGTATACGATTTATCC 720  
 DB 901 CTGCAACTACTTCTGCTCCCTGTGTGTGTGTGTGATGACACTTGTATACGATTTATCC 960  
 QY 721 ACACCTGACCAAGTGTGTGAGTTTGAAGCTGTGTGTGTGTGATCTTCACTG 780  
 DB 961 ACACCTGACCAAGTGTGTGAGTTTGAAGCTGTGTGTGTGTGATCTTCACTG 1020  
 QY 781 CCATTCTCTACTCTCTTCATTTTACATTTTATTTTACCTTCATATCTTGAGGGTCA 840  
 DB 1021 CCATTCTCTACTCTCTTCATTTTACATTTTATTTTACCTTCATATCTTGAGGGTCA 1080  
 QY 841 TTGGATGAAATCTTGCCTGCTTCATCAAGTTTGTTCATGAGATGAGATCATCATGAG 900  
 DB 1081 TTGGATGAAATCTTGCCTGCTTCATCAAGTTTGTTCATGAGATGAGATCATCATGAG 1140  
 QY 901 CTTCATGTTTCTTACCATTTAGTGTGTGTGTGTGATGACCTTTGTACTTACTATATG 960  
 DB 1141 CTTCATGTTTCTTACCATTTAGTGTGTGTGTGTGATGACCTTTGTACTTACTATATG 1200  
 QY 961 TGGTGTGAGGACAACTTTCAGCAGGCTGTGTGTGTGTGTGATGACCTTTGTACTTACTATATG 1020  
 DB 1201 TGGTGTGAGGACAACTTTCAGCAGGCTGTGTGTGTGTGTGATGACCTTTGTACTTACTATATG 1260  
 QY 1021 GGAACCTTGACCAAGCAAAATTTAGTACTCAAAACACCTTGAAATATTTCAATTA 1080  
 DB 1261 GGAACCTTGACCAAGCAAAATTTAGTACTCAAAACACCTTGAAATATTTCAATTA 1320  
 QY 1081 C 1081  
 DB 1321 C 1321

RESULT 4  
 ABV24026  
 ID ABV24026 standard; cDNA; 1729 BP.  
 XX AC ABV24026;  
 DE 16-SEP-2002 (first entry)  
 XX  
 DE Human prostate expression marker cDNA 24017.  
 XX  
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
 KW pharmacogenomic marker; gene; ss.  
 XX  
 OS Homo sapiens.  
 PN  
 XX MO200160860-A2.  
 XX  
 PD 23-AUG-2001.  
 XX  
 PF 20-FEB-2001; 2001MO-US05171.  
 XX







Db 961 GTAAAGCGGAACTTGAGCAAGCAAAATAATTAGTACTCAACACACCTTGA 1014

RESULT 11  
LOCUS AB083598 1014 bp DNA linear PRI 24-MAY-2002  
DEFINITION Homo sapiens GPCR gene for putative G-protein coupled receptor, complete cds, clone:hGPCR16.  
ACCESSION AB083598  
VERSION AB083598.1 GI:20152259  
KEYWORDS  
SOURCE Homo sapiens DNA, clone:hGPCR16.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
AUTHORS 1  
Takeda, S., Kadowaki, S., Haga, T., Takeasu, H. and Mitaku, S.  
TITLE Identification of G protein-coupled receptor genes from the human genome sequence  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1014)  
Takeda, S., Kadowaki, S., Haga, T., Takeasu, H. and Mitaku, S.  
AUTHORS Direct Submission  
JOURNAL Submitted (10-APR-2002) Shigeaki Takeda, Gunma University, Department of Biological and Chemical Engineering, Faculty of Engineering, 1-5-1, Kiryu, Gunma 376-8515, Japan  
(E-mail:stakeda@ce.gunma-u.ac.jp, Tel:+81-277-30-1434, Fax:+81-277-30-1434)

FEATURES  
source  
1..1014  
location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="hGPCR16"  
1..1014  
/gene="GPCR"  
1..1014  
/gene="GPCR"  
/note="predicted with SOSUI analysis"  
/codon\_start=1  
/product="putative G-protein coupled receptor"  
/protein\_id="BAB89311.1"  
/db\_xref="gi:20152260"  
/translation="MNEPLDYLANSDPEVAAARGNCTDENIPKMHVLPVYGLIF  
LVGRGNAVISTYIFKRPKPKSSTIIMNLACTDLITSLPIIHHYVASENNITG  
DFPKFIKFSFENLYSSILFLKPSIRCVIIHPMSCFSLHKTRCAVAVWII  
SLVAVIPMTFLITSTNRNSACLDLTSDELITIKYNLLITLITPLIVITVLY  
TIIHTEHGLTDSCLKOKARPLTILLILFYVCFPLIIRIVRISRLISCSL  
ENQHEAVIYSRPLAALNTFGLNLLIYVSDNFDQAVGSTRCKVSGMLEDAKISYS  
NMP"

BASE COUNT 258 a 263 c 189 g 304 t  
ORIGIN

Query Match 93.8%; Score 1014; DB 9; Length 1014;  
Best Local Similarity 100.0%; Pred. No. 2.7e-253; Indels 0; Gaps 0;  
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 ATGATGATGACCACTAGACTATTATGCAAAATGCTTGATTTCCCGATATGACGTGCT 113  
Db 1 ATGATGATGACCACTAGACTATTATGCAAAATGCTTGATTTCCCGATATGACGTGCT 60  
Qy 114 TTGTGAAATGCACTGATGAAAACATCCCACTCAAGATGACCTACCTCCCTGTATTAT 173  
Db 61 TTGTGAAATGCACTGATGAAAACATCCCACTCAAGATGACCTACCTCCCTGTATTAT 120  
Qy 174 GGCAATATCTCTCGTGGGATTTCCAGGCAATGAGTAGATATCCACTCAATTTTC 233  
Db 121 GGCAATATCTCTCGTGGGATTTCCAGGCAATGAGTAGATATCCACTCAATTTTC 180  
Qy 234 AAATGAGACCTTGGAAGAGCAGCAGCATCATTTATGCTGACCTGGCCGACAGATCTG 293  
Db 181 AAATGAGACCTTGGAAGAGCAGCAGCATCATTTATGCTGACCTGGCCGACAGATCTG 240

Qy 294 CTGTATCTGACCAAGCTCCCTTCCGATTCATCTATGACAGTGGCGAAAATGAGATC 353  
Db 241 CTGTATCTGACCAAGCTCCCTTCCGATTCATCTATGACAGTGGCGAAAATGAGATC 300  
Qy 354 TTGTGAGATTTTCAATGTAAGTTTATCGCTTCAGCTTCATTTCAACCTGTATGACAGC 413  
Db 301 TTGTGAGATTTTCAATGTAAGTTTATCGCTTCAGCTTCATTTCAACCTGTATGACAGC 360  
Qy 414 ATCCCTTCCCTCAACCTGTTCAGCATCTTCCGCTACTGTGTATCATTTCAACCAATGAGC 473  
Db 361 ATCCCTTCCCTCAACCTGTTCAGCATCTTCCGCTACTGTGTATCATTTCAACCAATGAGC 420  
Qy 474 TCGTTTCATTCACAAAACCTGATGATGAGTGTAGCCGCTGCTGGTGGATGATCAT 533  
Db 421 TCGTTTCATTCACAAAACCTGATGATGAGTGTAGCCGCTGCTGGTGGATGATCAT 480  
Qy 534 TCACTGTAGCTGTCAATTCGATGACCTTCCTTATCATCACTCAACCAAGACAGAGAG 593  
Db 481 TCACTGTAGCTGTCAATTCGATGACCTTCCTTATCATCACTCAACCAAGACAGAGAG 540  
Qy 594 TCACTGTAGCTGTCAATTCGATGACCTTCCTTATCATCACTCAACCAAGACAGAGAG 653  
Db 541 TCACTGTAGCTGTCAATTCGATGACCTTCCTTATCATCACTCAACCAAGACAGAGAG 600  
Qy 654 ATTTGACATGCAACTACTTCTGCGCCCTGCTGGTGTAGTGTAGCACTTTGCTATACAGC 713  
Db 601 ATTTGACATGCAACTACTTCTGCGCCCTGCTGGTGTAGTGTAGCACTTTGCTATACAGC 660  
Qy 714 ATTTGACATGCAACTACTTCTGCGCCCTGCTGGTGTAGTGTAGCACTTTGCTATACAGC 773  
Db 661 ATTTGACATGCAACTACTTCTGCGCCCTGCTGGTGTAGTGTAGCACTTTGCTATACAGC 720  
Qy 774 AGGCTTACCATTTCTGCTACTCTTGTGATTTTACGATGTTTATACCTTCCATATCTTG 833  
Db 721 AGGCTTACCATTTCTGCTACTCTTGTGATTTTACGATGTTTATACCTTCCATATCTTG 780  
Qy 834 AGGCTTACCATTTCTGCTACTCTTGTGATTTTACGATGTTTATACCTTCCATATCTTG 893  
Db 781 AGGCTTACCATTTCTGCTACTCTTGTGATTTTACGATGTTTATACCTTCCATATCTTG 840  
Qy 894 CATGAGCTTACATGTTTCTAGACCATATGCTGCTGACACCTTTGGTAACTGTTA 953  
Db 841 CATGAGCTTACATGTTTCTAGACCATATGCTGCTGACACCTTTGGTAACTGTTA 900  
Qy 954 CATATGCTGTGTGACGACAACTTTTACAGAGCTGTCTGCTCAACAGTGAATGCAAA 1013  
Db 901 CATATGCTGTGTGACGACAACTTTTACAGAGCTGTCTGCTCAACAGTGAATGCAAA 960  
Qy 1014 GTAAAGCGGAACTTGAGCAAGCAAAATAATTAGTACTCAACACACCTTGA 1067  
Db 961 GTAAAGCGGAACTTGAGCAAGCAAAATAATTAGTACTCAACACACCTTGA 1014

RESULT 12  
LOCUS AF411109 1014 bp DNA linear PRI 01-NOV-2001  
DEFINITION Homo sapiens G protein-coupled receptor (GPR80) gene, complete cds.  
ACCESSION AF411109  
VERSION AF411109.1 GI:16566322  
KEYWORDS  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
AUTHORS 1  
Lee, D.K., Nguyen, T., Lynch, K.R., Cheng, R., Vantli, W.B., Arkhitekt, O., Lewis, T., Evans, J.F., George, S.R. and O'Dowd, B.F.  
TITLE Discovery and mapping of ten novel G protein-coupled receptor genes  
JOURNAL Gene 275 (1), 83-91 (2001)  
MEDLINE 21458557  
PUBMED 11574155  
REFERENCE 2 (bases 1 to 1014)  
AUTHORS Lee, D.K., Nguyen, T., Lynch, K.R., Cheng, R., Vantli, W.B., Arkhitekt, O.,

QY 1056 AACAACTTGAATATTTTCAATTAC 1081  
 DB 1021 AACAACTTGAATATTTTCAATTAC 1046  
 RESULT 8  
 LOCUS AX148186 1014 bp DNA linear PAT 08-JUN-2001  
 DEFINITION Sequence 27 from Patent WO0136471.  
 ACCESSION AX148186  
 VERSION AX148186.1 GI:14347086  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE  
 1 (Bases 1 to 1014)  
 Chen, R., Dang, H.T. and Lowitz, K.P.  
 Endogenous and non-endogenous versions of human g protein-coupled  
 receptors  
 JOURNAL Patent: WO 0136471-A 27 25-MAY-2001;  
 Arena Pharmaceuticals, Inc. (US)  
 FEATURES  
 source 1..1014  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 ORIGIN  
 BASE COUNT 258 a 263 c 189 g 304 t  
 ORIGIN  
 Query Match 93.8%; Score 1014; DB 6; Length 1014;  
 Best Local Similarity 100.0%; Pred. No. 2,7e-253;  
 Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 54 ATGATGAGCCACTGACTATTTAGCAAAATGCTTCTGATTTCCCGATTATGACGTCT 113  
 DB 1 ATGATGAGCCACTGACTATTTAGCAAAATGCTTCTGATTTCCCGATTATGACGTCT 60  
 QY 114 TTGGAAATTCGACATGATGAAGCAATCCCACTCAAGATGCACTACCTCCCTGATTTAT 173  
 DB 61 TTGGAAATTCGACATGATGAAGCAATCCCACTCAAGATGCACTACCTCCCTGATTTAT 120  
 QY 174 GGCATTATCTCTCTGCGGATTTCCAGGCAATGAGTAGATATTCATTAATTTTC 233  
 DB 121 GGCATTATCTCTCTGCGGATTTCCAGGCAATGAGTAGATATTCATTAATTTTC 180  
 QY 234 AAAATGAGACCTTGGAGAGGACGACCATATTATGCTGAACCTGGCTGCAAGATCTG 293  
 DB 181 AAAATGAGACCTTGGAGAGGACGACCATATTATGCTGAACCTGGCTGCAAGATCTG 240  
 QY 294 CTGATCTGACCAAGCTCCCTCTCTGATTCATGACTATGCAATGCGAAGCAAACTGGATC 353  
 DB 241 CTGATCTGACCAAGCTCCCTCTCTGATTCATGACTATGCAATGCGAAGCAAACTGGATC 300  
 QY 354 TTGGAGATTCATGATGATGAATTTATCCGCTTCAGCTTCATTTCAACTGATAGCAGC 413  
 DB 301 TTGGAGATTCATGATGATGAATTTATCCGCTTCAGCTTCATTTCAACTGATAGCAGC 360  
 QY 414 ATCTCTCTCTCACTGTTTTCAGCATCTTCCGCTACTGCTGATCATTTCAACCAATGAGC 473  
 DB 361 ATCTCTCTCTCACTGTTTTCAGCATCTTCCGCTACTGCTGATCATTTCAACCAATGAGC 420  
 QY 474 TGCTTTTTCATTCACAAAAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 533  
 DB 421 TGCTTTTTCATTCACAAAAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 480  
 QY 534 TCACCTGAGTGTGATATTCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 593  
 DB 481 TCACCTGAGTGTGATATTCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 540  
 QY 594 TCACCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 653  
 DB 541 TCACCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600

QY 654 ATTTGACTGCAACTACTTCTGCTCCCTGATGATGATGATGATGATGATGATGATGATGAT 713  
 DB 601 ATTTGACTGCAACTACTTCTGCTCCCTGATGATGATGATGATGATGATGATGATGATGAT 660  
 QY 714 ATTATCCACACTCTGACCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 773  
 DB 661 ATTATCCACACTCTGACCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720  
 QY 774 AGGCTAACCATCTGCTACTCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 833  
 DB 721 AGGCTAACCATCTGCTACTCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 780  
 QY 834 AGGCTAACCATCTGCTACTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 893  
 DB 781 AGGCTAACCATCTGCTACTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 840  
 QY 894 CATGAGCTTACATGCTGTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 953  
 DB 841 CATGAGCTTACATGCTGTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
 QY 954 CATGAGCTTACATGCTGTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1013  
 DB 901 CATGAGCTTACATGCTGTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 960  
 QY 1014 GTAAAGCGGAACTTGGAGAGCAAGCAAAATTTAGTACTCAACCAACCTTGA 1067  
 DB 961 GTAAAGCGGAACTTGGAGAGCAAGCAAAATTTAGTACTCAACCAACCTTGA 1014  
 RESULT 9  
 LOCUS AX379468 1014 bp DNA linear PAT 18-MAR-2002  
 DEFINITION Sequence 1 from Patent WO0187980.  
 ACCESSION AX379468  
 VERSION AX379468.1 GI:19575226  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE  
 1  
 Wei, M.H., Zhao, Q.C., Cravchik, A.C., di Francesco, V.C. and  
 Beasley, B.M.  
 TITLE Isolated human g-protein coupled receptors, nucleic acid molecules  
 encoding human gpcr proteins, and uses thereof  
 JOURNAL Patent: WO 0187980-A 1 22-NOV-2001;  
 Applera Corporation Robert A. Millman Assistant Secretary (US)  
 FEATURES  
 source 1..1014  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 BASE COUNT 258 a 263 c 189 g 304 t  
 ORIGIN  
 Query Match 93.8%; Score 1014; DB 6; Length 1014;  
 Best Local Similarity 100.0%; Pred. No. 2,7e-253;  
 Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 54 ATGATGAGCCACTGACTATTTAGCAAAATGCTTCTGATTTCCCGATTATGACGTCT 113  
 DB 1 ATGATGAGCCACTGACTATTTAGCAAAATGCTTCTGATTTCCCGATTATGACGTCT 60  
 QY 114 TTGGAAATTCGACATGATGAAGCAATCCCACTCAAGATGCACTACCTCCCTGATTTAT 173  
 DB 61 TTGGAAATTCGACATGATGAAGCAATCCCACTCAAGATGCACTACCTCCCTGATTTAT 120  
 QY 174 GGCATTATCTCTCTGCGGATTTCCAGGCAATGAGTAGATATTCATTAATTTTC 233  
 DB 121 GGCATTATCTCTCTGCGGATTTCCAGGCAATGAGTAGATATTCATTAATTTTC 180  
 QY 234 AAAATGAGACCTTGGAGAGGACGACCATATTATGCTGAACCTGGCTGCAAGATCTG 293  
 DB 181 AAAATGAGACCTTGGAGAGGACGACCATATTATGCTGAACCTGGCTGCAAGATCTG 240

D	b	140435	TGACCAAGCTCCCTTCTTGATTCACACTAATGCAGTGGCGAAACCTGAATCTTTGGAG	140494
Oy		361	ATTGTGATGTGAAGTTTATCCGCTTCAGCTTCATTTCAACCTGTATATAGCAGATCTCT	420
D	b	140495	ATTTCATGTGTGAAGTTTATCCGCTTAGCTTCATTTCAACCTGTATATAGCAGATCTCT	140554
Oy		421	TCCTCAAGCTGTTTCAGACATCTTCCGCTACGTGTGTGATCAATTCACCATAGAGCTGTTT	480
D	b	140555	TCCTCAAGCTGTTTCAGACATCTTCCGCTACGTGTGTGATCAATTCACCATAGAGCTGTTT	140614
Oy		481	CCATTCACAAAAGCTGATGTGAGAGTTGTAGCCGTGTGTCGTGTGGTGTGATCATTTTCACTGG	540
D	b	140615	CCATTCACAAAAGCTGATGTGAGAGTTGTAGCCGTGTGTCGTGTGGTGTGATCATTTTCACTGG	140674
Oy		541	TAGCTGTCAATTCGAGATGACCTTCTTGATCACATCAACAAGSACCAAGATCAGCT	600
D	b	140675	TAGCTGTCAATTCGAGATGACCTTCTTGATCACATCAACAAGSACCAAGATCAGCT	140734
Oy		601	GTTCTGACCTCAACCAAGTTGGATGAATCTCAATATATTAATGTGTCAAACCTGATTTTGA	660
D	b	140735	GTTCTGACCTCAACCAAGTTGGATGAATCTCAATATATTAATGTGTCAAACCTGATTTTGA	140794
Oy		661	CTGCAACTATCTTTCGCCCTCCCTGGTGTGTGTGTGACATTTTGCTATACCAAGATTAATCC	720
D	b	140795	CTGCAACTATCTTTCGCCCTCCCTGGTGTGTGTGTGACATTTTGCTATACCAAGATTAATCC	140854
Oy		721	ACACTCTGACCCATGGAAGCTGCAAACTGACAGCTGCTTAAGCAGAAAGCAGAAGGCTTA	780
D	b	140855	ACACTCTGACCCATGGAAGCTGCAAACTGACAGCTGCTTAAGCAGAAAGCAGAAGGCTTA	140914
Oy		781	CCATTCGTGCTACTCTCTTGATTTTAACGATGTTTTTAACTCTTCATATCTTGAGGGTCA	840
D	b	140915	CCATTCGTGCTACTCTCTTGATTTTAACGATGTTTTTAACTCTTCATATCTTGAGGGTCA	140974
Oy		841	TTCCGATGGAATCTGGCCCTGCTTCAATAGTGTTCCTATGGAATTCAGATCCATGAAG	900
D	b	140975	TTCCGATGGAATCTGGCCCTGCTTCAATAGTGTTCCTATGGAATTCAGATCCATGAAG	141034
Oy		901	CTTACATGCTTTCTAGAACCATTAGCTGCTGTGAAACAACCTTTGGTAACTGTACTATATG	960
D	b	141035	CTTACATGCTTTCTAGAACCATTAGCTGCTGTGAAACAACCTTTGGTAACTGTACTATATG	141094
Oy		961	TGTGTGTGACGACAACTTTTCAGCAGAGCTGTCTGCTCAACAGTGTGATSCAAAGTAAGCG	1020
D	b	141095	TGTGTGTGACGACAACTTTTCAGCAGAGCTGTCTGCTCAACAGTGTGATSCAAAGTAAGCG	141154
Oy		1021	GGAACCTTGAGAGCAAGAAATAATGTTACTCAAAACAACCTTGAATATTTCAATTTA	1080
D	b	141155	GGAACCTTGAGAGCAAGAAATAATGTTACTCAAAACAACCTTGAATATTTCAATTTA	141214
Oy		1081	C 1081	
D	b	141215	C 141215	
RESULT 6				
AXI91332		1729 bp	DNA	linear PAT 15-AUG-2001
LOCUS				
DEFINITION		Sequence 2 from Patent WO0149847.		
ACCESSION		AXI91332		
VERSION		AXI91332.1		GI:15209582
KEYWORDS				
SOURCE		human.		
ORGANISM		Homo sapiens		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE		Glucksmann,M.A. and White,D.		
JOURNAL		26004, 38911, and 39404, seven-transmembrane proteins / g-protein		
		coupled receptors		
		Patent: WO 0149847-A 2 12-JUL-2001;		
		Millennium Pharmaceuticals,Inc. (US)		

FEATURES	Location/Qualifiers
source	1. .1729 /organism="Homo sapiens" /db_xref="taxon:9606" 294 . .1307 /note="unnamed protein product"
CDS	/codon_start=1 /protein_id="CAC51133.1" /db_xref="GI:15209583" /translation="MNPEPLDYLANASDFPDYAAAFNGCNDENILPMKHYLPVYIGIIF LVDFPGNAVVISIVYIFKMRPMWSSSTIIMNLACTDILYLSPELILHYVAGSNMIFG DMPCKPIRSEFHNLYSSILFPLCFSEIFRVCVLIHMSCSIHKTKCAVACAVMIT SLVAIVPMFPLITSTNKRNSACLDLSDSLIMKYNILVTAFFCLPLVLTCLY TTIILHTGLQDSDCLKOKARLITLILAFVPCIPFIIILVILIESLISISCI ENIILHRAVIVSGPLAALNFGNLLLYVVSDFNQAVCSIVRCVSGNLEQAKKISYS NND"
BASE COUNT	461 a 403 c 302 g 563 t
ORIGIN	
Query Match	99.9%; Score 1079.4; DB 6; Length 1729;
Best Local Similarity	99.9%; Pred. No. 2.4e-270;
Matches 1080; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
Db	1 CATATTGCCAACTGAACTCTCTTGTGTTTCTTGCAAGATGAAGAGACAACATGAATG 60
Db	241 CATATTGCCAACTGAACTCTCTTGTGTTTCTTGCAAGATGAAGAGACAACATGAATG 300
Qy	61 AGCCACTGACTATTGTCGAAAGAGCTCTGATTTCCCGAGTTATGACAGCTGTTGGAA 120
Db	301 AGCCACTGACTATTGTCGAAAGAGCTCTGATTTCCCGAGTTATGACAGCTGTTGGAA 360
Qy	121 ATTGCACGTAGTAAAGACATCCCACTCAAGATGACCTACCTCCCTGTTATTATGACATTA 180
Db	361 ATTGCACGTAGTAAAGACATCCCACTCAAGATGACCTACCTCCCTGTTATTATGACATTA 420
Qy	181 TCTTCTCTGTGGGATTTTCAGGGCATGCAGTAGTGAATATCCATTACATTTCAAATGA 240
Db	421 TCTTCTCTGTGGGATTTTCAGGGCATGCAGTAGTGAATATCCATTACATTTCAAATGA 480
Qy	241 GACCTTGGAAGAGAGACCATCATTTATGCTGAACCTGGGCTGACAGATGCTGTATC 300
Db	481 GACCTTGGAAGAGAGACCATCATTTATGCTGAACCTGGGCTGACAGATGCTGTATC 540
Qy	301 TGACCAAGCTCCCTTCCTGATTCACACTACTATGCTAGTGGGAAAATGATCTTTGGAG 360
Db	541 TGACCAAGCTCCCTTCCTGATTCACACTACTATGCTAGTGGGAAAATGATCTTTGGAG 600
Qy	361 ATTTCATGTGTAACTTATCCGCTTCAGCTTCAATTTCAACTGTATAGCAGATCCTCT 420
Db	601 ATTTCATGTGTAACTTATCCGCTTCAGCTTCAATTTCAACTGTATAGCAGATCCTCT 660
Qy	421 TCCCTCACTGTTTAAAGATCTCCGCTACACTGTGTGATCATTCACCCATAGAGCTCTTT 480
Db	661 TCCCTCACTGTTTAAAGATCTCCGCTACACTGTGTGATCATTCACCCATAGAGCTCTTT 720
Qy	481 CCATTCAAAAACTCGATGTGTCAGTTTAGGCTGTGCTGTGATGATCATTTCACTGG 540
Db	721 CCATTCAAAAACTCGATGTGTCAGTTTAGGCTGTGCTGTGATGATCATTTCACTGG 780
Qy	541 TAGCTGTCAATCCGATGACCTCTTGTATCATCATCAACCAACAGGACCAAGATCAAGCT 600
Db	781 TAGCTGTCAATCCGATGACCTCTTGTATCATCATCAACCAACAGGACCAAGATCAAGCT 840
Qy	601 GTCGTGACCTCCACAGTTTGGATGTAACCTAACTATTAAGTGTATCAACTGATTTTGA 660
Db	841 GTCGTGACCTCCACAGTTTGGATGTAACCTAACTATTAAGTGTATCAACTGATTTTGA 900
Qy	661 CTGCAACTACTTTCTGCTCCCTCCCTGTGATGATGACACTTTGGTATATACCAGATATCC 720
Db	901 CTGCAACTACTTTCTGCTCCCTCCCTGTGATGATGACACTTTGGTATATACCAGATATCC 960
Qy	721 ACACCTTGACCCATGACCTGCAACTGACAGCTGCTTAAGACGAAAAGACGAAAGCTAA 780





